

FEATURES
source

Location/Qualifiers
1. 495
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S22SN016n1-150-D07"
/sex="F"
/tissue_type="Asciites"
/cell_type="Lymphoblast-like"
/cell_line="SN-16"
/lab_host="DH10B"
/clone_lib="S22SN016n1"
/note="Organ: Stomach; Vector: pT73-Pac; Site_1: EcoRI; Site_2: NotI; The S22SN016 library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cells of SN-16 culture. SN-16 cell was obtained from Korean Cell Line Bank (KCLB). SN-16 was established from ascitic fluids of Korean patients by Park J.G. et al. (1990), Cancer Res 50: 2773-2780."

BASE COUNT
107 a 169 c 134 g 85 t

Query Match
Best Local Similarity 100.0%; Score 216; DB 12; Length 495;
Pred. No. 9.8e-48;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCGCGCGCGCGCGAGGGGTGACATCCATCGAGGACAGCTCCAGCCATCTGGC 60
Db 39 CCGCGCGCGCGCGCGAGGGGTGACATCCATCGAGGACAGCTCCAGCCATCTGGC 98
QY 61 CAGGCGGTGACTGTCTCGAGGAGCCAGCCCTCAACGCTACACTGCAAGTGG 120
Db 99 CAGGCGGTGACTGTCTCGAGGAGCCAGCCCTCAACGCTACACTGCAAGTGG 158
QY 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGAGTACCCCAACCATCTTGTCC 180
Db 159 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGAGTACCCCAACCATCTTGTCC 218
QY 181 CTTCCACATCCATGATGAAGCCCAATGATGGGTGACA 216
Db 219 CTTCCACATCCATGATGAAGCCCAATGATGGGTGACA 254

RESULT 2
AV704776 496 bp mRNA linear EST 09-OCT-2000
LOCUS AV704776 ADB Homo sapiens CDNA clone ADBBUC04 5', mRNA sequence.
DEFINITION AV704776
ACCESSION AV704776.1 GI:10722088
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 496)
Peng, Y., Song, H., Huang, Q., Gu, Y., Yang, Y., Gao, G., Xiao
H., Xu, X., Li, N., Qian, B., Liu, F., Qu, X., Gao, X., Cheng, Z., Xu, Z.,
Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu
G., Hu, R., Chen, J., Chen, Z. and Han, Z.

TITLE
JOURNAL
COMMENT
Unpublished
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
1. 496
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ADBBUC04"
/tissue_type="Adrenal gland"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="ADB"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

BASE COUNT
107 a 178 c 131 g 80 t

Query Match
Best Local Similarity 100.0%; Score 216; DB 9; Length 496;
Pred. No. 9.8e-48;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCGCGCGCGCGCGAGGGGTGACATCCATCGAGGACAGCTCCAGCCATCTGGC 60
Db 181 CCGCGCGCGCGCGCGAGGGGTGACATCCATCGAGGACAGCTCCAGCCATCTGGC 240
QY 61 CAGGCGGTGACTGTCTCGAGGAGCCAGCCCTCAACGCTACACTGCAAGTGG 120
Db 241 CAGGCGGTGACTGTCTCGAGGAGCCAGCCCTCAACGCTACACTGCAAGTGG 300
QY 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGAGTACCCCAACCATCTTGTCC 180
Db 301 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGAGTACCCCAACCATCTTGTCC 360
QY 181 CTTCCACATCCATGATGAAGCCCAATGATGGGTGACA 216
Db 361 CTTCCACATCCATGATGAAGCCCAATGATGGGTGACA 396

RESULT 3
BU850016 815 bp mRNA linear EST 16-OCT-2002
LOCUS BU850016
DEFINITION AGENCOURT_10438272 NIH_MGC_109 Homo sapiens CDNA clone
IMAGE:6598770 5', mRNA sequence.
ACCESSION BU850016
VERSION BU850016.1 GI:24034979
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 815)
NIH-MGC http://mgc.ncl.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: L1CM2832 row: b column: 18
High quality sequence stop: 700.
Location/Qualifiers

FEATURES
source
1. 815
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6598770"
/tissue_type="teratocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_109"
/note="Organ: ovary; Vector: pOTB7; Site_1: EcoRI; Site_2: XhoI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:

1. 815
Location/Qualifiers

GGCAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC library."

BASE COUNT 236 a 271 c 172 g 136 t
 Query Match 100.0%; Score 216; DB 13; Length 815;
 Best Local Similarity 100.0%; Pred. No. 1.2e-47;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCGCGCCGCCCGAGAGGGGTGACCTCATCCAGGTCCCGAGCAGCTGGC 60
 |||||||
 DB 96 CCGCGCGCCGCCCGAGAGGGGTGACCTCATCCAGGTCCCGAGCAGCTGGC 155
 QY 61 CAGGCGGTGACTGTCTCGAGGAGCCCGCCTCAACGCTTACACTGACGAAGTGC 120
 |||||||
 DB 156 CAGGCGGTGACTGTCTCGAGGAGCCCGCCTCAACGCTTACACTGACGAAGTGC 215
 QY 121 GGGCTGAAGCGTACGCGCTCGTAAAGCGGAGCGTACCCCGAACCATCTTGTCTCC 180
 |||||||
 DB 216 GGGCTGAAGCGTACGCGCTCGTAAAGCGGAGCGTACCCCGAACCATCTTGTCTCC 275
 QY 181 CTTTCACATCCATGAGCCCAATGATGGGTGACA 216
 |||||||
 DB 276 CTTTCACATCCATGAGCCCAATGATGGGTGACA 311

RESULT 4
 BQ723018 862 bp mRNA linear EST 16-JUL-2002
 LOCUS AGENCOURT 8099701 lupski_sympathetic_trunk Homo sapiens cDNA clone
 DEFINITION IMAGE:6190272 5', mRNA sequence.

ACCESSION BQ723018
 VERSION BQ723018.1 GI:21861915
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 862)
 NIH-MGC http://mgc.ncl.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov

Tissue Procurement: Dr. James R. Lupski
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1AM13588 row: n column: 01
 High quality sequence stop: 592.

FEATURES

source
 1. 862
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6190272"
 /sex="male"
 /tissue_type="sympathetic trunk"
 /dev_stage="adult, 16 yr"
 /lab_host="DH10B"
 /clone_lib="lupski_sympathetic_trunk"
 /note="Vector: PCMV-SF0R6 (Life Technologies); Site_1:
 Note: Site 2: SalI; cDNA made by oligo-dT priming.
 directionally cloned using the following adaptors:
 5'-GACATGTTAGATCGCAGGCGCGCCCT(15)-3'. Size selected >
 1 kb for average insert length 1.9 kb. This is a primary

library, non-amplified. Library constructed by Life technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life Technologies."

BASE COUNT 208 a 307 c 207 g 140 t
 Query Match 100.0%; Score 216; DB 13; Length 862;
 Best Local Similarity 100.0%; Pred. No. 1.2e-47;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCGCGCCGCCCGAGAGGGGTGACCTCATCCAGGTCCCGAGCAGCTGGC 60
 |||||||
 DB 269 CCGCGCGCCGCCCGAGAGGGGTGACCTCATCCAGGTCCCGAGCAGCTGGC 328
 QY 61 CAGGCGGTGACTGTCTCGAGGAGCCCGCCTCAACGCTTACACTGACGAAGTGC 120
 |||||||
 DB 329 CAGGCGGTGACTGTCTCGAGGAGCCCGCCTCAACGCTTACACTGACGAAGTGC 388
 QY 121 GGGCTGAAGCGTACGCGCTCGTAAAGCGGAGCGTACCCCGAACCATCTTGTCTCC 180
 |||||||
 DB 389 GGGCTGAAGCGTACGCGCTCGTAAAGCGGAGCGTACCCCGAACCATCTTGTCTCC 448
 QY 181 CTTTCACATCCATGAGCCCAATGATGGGTGACA 216
 |||||||
 DB 449 CTTTCACATCCATGAGCCCAATGATGGGTGACA 484

RESULT 5
 BE898612 928 bp mRNA linear EST 29-SEP-2000
 LOCUS BE898612
 DEFINITION mRNA sequence.

ACCESSION BE898612
 VERSION BE898612.1 GI:10365266
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 928)
 NIH-MGC http://mgc.ncl.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov

Tissue Procurement: DCTD/DP
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: L1CM820 row: c column: 14
 High quality sequence stop: 794.

FEATURES

source
 1. 928
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3951685"
 /tissue_type="adenocarcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH-MGC 9"
 /note="Organ: ovary; Vector: pORF7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCAGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 100.0%; Score 216; DB 10; Length 928;
 Best Local Similarity 100.0%; Pred. No. 1.2e-47;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCCGCCCCCGCCAGAGGGGTGACTTCATCCAGGTGCACAGCTCCAGCCATCTGGC 60
 |||||||
 DB 243 CCGCCGCCCCCGCCAGAGGGGTGACTTCATCCAGGTGCACAGCTCCAGCCATCTGGC 302
 |||||||
 QY 61 CAGGCGGTGACTGTCTCGAGGAGCCCGCCAGCCCTCAAGCCCTACACTGACAGGTGC 120
 |||||||
 DB 303 CAGGCGGTGACTGTCTCGAGGAGCCCGCCAGCCCTCAAGCCCTACACTGACAGGTGC 362
 |||||||
 QY 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGAGCTACCCCAACCAATCCTTGTCTCC 180
 |||||||
 DB 363 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGAGCTACCCCAACCAATCCTTGTCTCC 422
 |||||||
 QY 181 CTTCCACATCCATGAAGCCCAATGATGGGTGTACA 216
 |||||||
 DB 423 CTTCCACATCCATGAAGCCCAATGATGGGTGTACA 458
 |||||||

RESULT 6
 BE899378 1013 bp mRNA linear EST 29-SEP-2000
 LOCUS 601681309P1 NIH_MGC_9 Homo sapiens CDNA clone IMAGE:3951266 5',
 mRNA sequence.
 ACCESSION BE899378
 VERSION BE899378.1 GI:10367019
 KEYWORDS EST
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 1013)
 NIH-MGC <http://mgi.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: csapbs-remail.nih.gov
 Tissue Procurement: DCTD/DMP
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov
 Plate: L10CM819 row: b column: 03
 High quality sequence start: 30
 High quality sequence stop: 828.
 Location/Qualifiers

FEATURES

Source

1..1013
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3951266"
 /tissue_type="adenocarcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="NIH_MGC_9"
 /note="Organ: ovary; Vector: pOT87; Site: 1: XhoI; Site: 2:
 EcoRI; CDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCAGCAG(5). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-CDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 BASE COUNT 270 a 322 c 263 g 158 t
 ORIGIN

Query Match 100.0%; Score 216; DB 10; Length 1013;
 Best Local Similarity 100.0%; Pred. No. 1.2e-47;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCCGCCCCCGCCAGAGGGGTGACTTCATCCAGGTGCACAGCTCCAGCCATCTGGC 60
 |||||||
 DB 292 CCGCCGCCCCCGCCAGAGGGGTGACTTCATCCAGGTGCACAGCTCCAGCCATCTGGC 351
 |||||||
 QY 61 CAGGCGGTGACTGTCTCGAGGAGCCCGCCAGCCCTCAAGCCCTACACTGACAGGTGC 120
 |||||||
 DB 352 CAGGCGGTGACTGTCTCGAGGAGCCCGCCAGCCCTCAAGCCCTACACTGACAGGTGC 411
 |||||||
 QY 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGAGCTACCCCAACCAATCCTTGTCTCC 180
 |||||||
 DB 412 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGAGCTACCCCAACCAATCCTTGTCTCC 471
 |||||||
 QY 181 CTTCCACATCCATGAAGCCCAATGATGGGTGTACA 216
 |||||||
 DB 472 CTTCCACATCCATGAAGCCCAATGATGGGTGTACA 507
 |||||||

RESULT 7
 N31401 494 bp mRNA linear EST 10-JAN-1996
 LOCUS YX67d08.r1 Soares melanocyte 2NbhM Homo sapiens CDNA clone
 IMAGE:26679 5', mRNA sequence.
 ACCESSION N31401
 VERSION N31401.1 GI:1151800
 KEYWORDS EST
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 494)
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman,
 M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
 Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston,
 R., Williamson, A., Wohlmann, P. and Wilson, R.
 The WashU-Merck EST Project
 Unpublished
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence stops: 464
 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (infoimage.llnl.gov) for further information.
 Seq primer: T7
 High quality sequence stop: 464.
 Location/Qualifiers

FEATURES

Source

1..494
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:3876441"
 /db_xref="taxon:9606"
 /clone="IMAGE:266799"
 /sex="Male"
 /tissue_type="melanocyte"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_id="Soares melanocyte 2NbhM"
 /note="Vector: pT7T3 (Pharmacia) with a modified
 polylinker; Site: 1: Not I; Site: 2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5',
 TGTATCCATCTGAAGTGGGCGGCGGCACTTTTCTTTTCTTTT 3'], RI
 double-stranded cDNA was size selected, ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT7T3 vector
 (Pharmacia). Library constructed by Bento Soares and
 M. Patricia Bonaldo. RNA from normal foreskin melanocytes
 (FS374) was kindly provided by Dr. Anthony P. Albino."
 BASE COUNT 110 a 165 c 131 g 83 t
 ORIGIN

Query Match 99.5%; Score 215; DB 14; Length 494;

Best Local Similarity 99.5%; Pred. No. 1.8e-47;
Matches 215; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGCCGCCGCCGCCGAGAGGGTGGAGCTCCATCCAGTGGACAGCTCCGCCAGCCATCTGGC 60
DB 60 CCGCCGCCGCCGCCGAGAGGGTGGAGCTCCATCCAGTGGACAGCTCCGCCAGCCATCTGGC 119
QY 61 CAGGCGGTGACTGTCTCGAGGAGAGCCGCTCAACGCTCAACTCACTGACAGAGTGC 120
DB 120 CAGGCGGTGACTGTCTCGAGGAGAGCCGCTCAACGCTCAACTCACTGACAGAGTGC 179
QY 121 GGGCTGAAGCGTAGCGCTCGCTTAAGCGGAGCTGACCCGCAACCATCTCTTCTGCC 180
DB 180 GGGCTGAAGCGTAGCGCTCGCTTAAGCGGAGCTGACCCGCAACCATCTCTTCTGCC 239
QY 181 CTTTCCACATCCATGAGAGCCCAATGATGCGTGTACA 216
DB 240 CTTTCCACATCCATGAGAGCCCAATGATGCGTGTACA 275

RESULT 8

BC032619 6875 bp mRNA linear HTC 04-MAR-2003
DEFINITION Homo sapiens, similar to sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A, clone IMAGE:5578066, mRNA.
ACCESSION BC032619
KEYWORDS
SOURCE HTC.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK

COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-rt@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nih.gov

Akher, N., Ayala, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dierlich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R., Madsen, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stanirip, S., Thomas, P.J., Touchman, J.W., Tsugeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L., H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Series: IRAC Plate: 69 Row: 0 Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 11915659
This clone has the following problem: retained intron.

FEATURES

source
1..6875
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5578066"
/tissue_type="Skin, melanotic melanoma."
/clone_lib="NIH_MGC_72"

/lab_host="DH10B"
/note="vector: PCMV-SPOK6"
BASE COUNT 1784 a 1795 c 1592 g 1704 t
ORIGIN

Query Match
Best Local Similarity 99.1%; Score 212.8; DB 11; Length 6875;
Matches 214; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCGCCGCCGCCGCCGAGAGGGTGGAGCTCCATCCAGTGGACAGCTCCGCCAGCCATCTGGC 60
DB 366 CCGCCGCCGCCGCCGAGAGGGTGGAGCTCCATCCAGTGGACAGCTCCGCCAGCCATCTGGC 3725
QY 61 CAGGCGGTGACTGTCTCGAGGAGAGCCGCTCAACGCTCAACTCACTGACAGAGTGC 120
DB 3726 CAGGCGGTGACTGTCTCGAGGAGAGCCGCTCAACGCTCAACTCACTGACAGAGTGC 3785
QY 121 GGGCTGAAGCGTAGCGCTCGCTTAAGCGGAGCTGACCCGCAACCATCTCTTCTGCC 180
DB 3786 GGGCTGAAGCGTAGCGCTCGCTTAAGCGGAGCTGACCCGCAACCATCTCTTCTGCC 3845
QY 181 CTTTCCACATCCATGAGAGCCCAATGATGCGTGTACA 216
DB 3846 CTTTCCACATCCATGAGAGCCCAATGATGCGTGTACA 3881

RESULT 9

N25829 462 bp mRNA linear EST 29-DEC-1995
LOCUS N25829
DEFINITION yx22d01.r1 Soares melanocyte 2nbhm Homo sapiens CDNA clone
ACCESSION N25829
IMAGE:262465 5', mRNA sequence.
VERSION N25829
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Maria, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished
CONTACT: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
High quality sequence stops: 360
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 117 Std Error: 0.00
Seq primer: T7
High quality sequence stop: 360.

FEATURES

source
1..462
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3872107"
/db_xref="taxon:9606"
/clone="IMAGE:262465"
/sex="Male"
/tissue_type="melanocyte"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares melanocyte 2nbhm"
/note="vector: p773D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand CDNA was primed with a Not I - oligo(dT) primer [5',
TGTACCAATCGAAGTGGAGCGGCCGACGTTTCTTTTCTTTT 3'],

double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo. RNA from normal foreskin melanocytes
(FS374) was kindly provided by Dr. Anthony P. Albino."

BASE COUNT 111 a 167 c 103 g 77 t 4 others
ORIGIN

Query Match 98.1%; Score 212; DB 14; Length 462;
Best Local Similarity 98.1%; Pred. No. 1.1e-46;
Matches 212; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGCGCGCCCGCCGAGAGGGTGGACTGCATCCAGTGCAGCTCCAGCCATCTGAC 60
DB 238 CGCGCGCCCGCCGAGAGGGTGGACTGCATCCAGTGCAGCTCCAGCCATCTGAC 297
QY 61 CAGCGCGTGTCTGTGAGGAGCCCAAGCCTCAAGCCTCACTCACTCAAGTGC 120
DB 238 CAGCGCGTGTCTGTGAGGAGCCCAAGCCTCAAGCCTCACTCACTCAAGTGC 357
QY 121 GGGCTGAAGCGTACCGCTCGGTAAAGCGGAGTACCCCAACCATCTCTGCTGCC 180
DB 358 GGGCTGAAGCGTACCGCTCGGTAAAGCGGAGTACCCCAACCATCTCTGCTGCC 417
QY 181 CTTTCACATCCATGAGCCCAATGATGCTGTACA 216
DB 418 CTTTCACATCCATGAGCCCAATGATGCTGTACA 453

RESULT 10

N46020 410 bp mRNA linear EST 14-FEB-1996
LOCUS yj3a05.r1 Soares melanocyte 2Nbhm Homo sapiens cDNA clone
DEFINITION IMAGE:273200 5', mRNA sequence.
ACCESSION N46020
VERSION N46020.1 GI:1187186
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 410)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston
, R., Williamson, A., Wohldmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LIND; contact the
IMAGE Consortium (info@image.lind.gov) for further information.
Seq primer: T7
High quality sequence stop: 329.
Location/Qualifiers
1..410
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3882842"
/db_xref="taxon:9606"
/clone="IMAGE:273200"
/sex="Male"
/tissue_type="melanocyte"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares melanocyte 2Nbhm"
/note="Vector: pT73D (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'

FEATURES

source

TTTACCAATCTGAGTGGAGCGGCGGAGTTTCTTTTCTTTT 3'},
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo. RNA from normal foreskin melanocytes
(FS374) was kindly provided by Dr. Anthony P. Albino."

BASE COUNT 99 a 143 c 101 g 62 t 5 others
ORIGIN

Query Match 94.3%; Score 203.6; DB 14; Length 410;
Best Local Similarity 98.1%; Pred. No. 1.9e-44;
Matches 206; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CCGCGCCCGAGAGGGTGGACTGCATCCAGTGCAGCTCCAGCCATCTGAC 66
DB 78 CCGCGCCCGAGAGGGTGGACTGCATCCAGTGCAGCTCCAGCCATCTGAC 137
QY 67 GTGACTGTCTGAGGAGCGCCAGCTCAAGCGCTCAACTCACTGACAGTGGGGCTG 126
DB 138 GTGACTGTCTGAGGAGCGCCAGCTCAAGCGCTCAACTCACTGACAGTGGGGCTG 197
QY 127 AAGCTACGCGCTGCTTAAAGCGGAGTACCCCAACCATCTCTGCTTTC 186
DB 198 AAGCTACGCGCTGCTTAAAGCGGAGTACCCCAACCATCTCTGCTTTC 257
QY 187 ACATCATGAAGCCCAATGATGCTGTACA 216
DB 258 ACATCATGAAGCCCAATGATGCTGTACA 287

RESULT 11

CB577257 632 bp mRNA linear EST 03-APR-2003
LOCUS CB577257
DEFINITION AMGNNUC:CDR91-00015-910-A cdr91 (10898) Rattus norvegicus cDNA
ACCESSION CB577257
VERSION CB577257.1 GI:29521298
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 632)
Amgen EST Program
Amgen Rat EST Program
Unpublished
COMMENT Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00015 row: 9 column: 10.
Location/Qualifiers
1..632
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="cdr91-00015-910"
/tissue_type="Chung Model Ipsilate"
/clone_lib="cdr91 (10898)"
/note="Vector: pSPORT1; Chung Model Rat DRG Left L5/L6"

FEATURES

source

Query Match 89.6%; Score 193.6; DB 14; Length 632;
Best Local Similarity 93.5%; Pred. No. 1.1e-41;
Matches 202; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 CGCGCGCCCGCCGAGAGGGTGGACTGCATCCAGTGCAGCTCCAGCCATCTGAC 60
DB 20 CCACCTCCGCGCCGAGAGGGTGGACTGCATCCAGTGCAGCTCCAGCCATCTGAC 79

QY 181 CTTCCACATCCATGAAGCCCATGATGCGTGTA 216
 |||||
 Db 1520 CTTCCACATCCATGAAGCCCATGATGCGTGTA 1555

use as a potential drug target
 JOURNAL Parent: WO 0031252-A 3 02-JUN-2000;
 KLOSTERMANN ANDREAS (DE) ; MAX PLANCK GESELLSCHAFT (DE) ; BEHL
 CHRISTIAN (DE)

FEATURES
 source Location/Qualifiers

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BASE COUNT 45 a 85 c 51 g 35 t
 ORIGIN

Query Match 100.0%; Score 216; DB 6; Length 216;
 Best Local Similarity 100.0%; Pred. No. 1.1e-41;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCCGCCGCCGCCGAGAGGGTGACTCCATCCAGGTGCACAGCTCCAGCCATCTGGC 60
 DB 1 CCGCCGCCGCCGCCGAGAGGGTGACTCCATCCAGGTGCACAGCTCCAGCCATCTGGC 60
 QY 61 CAGGCCGTGACTGTCTCGAGGAGGAGCCGCTCAAGCGCTCAACCTCACTGACAGAGTGC 120
 DB 61 CAGGCCGTGACTGTCTCGAGGAGGAGCCGCTCAAGCGCTCAACCTCACTGACAGAGTGC 120
 QY 121 GGGCTGAAGCGTAGCGCCCTCGCTAAAGCGGAGAGTACCCCAACCAATCCTTGGCTCC 180
 DB 121 GGGCTGAAGCGTAGCGCCCTCGCTAAAGCGGAGAGTACCCCAACCAATCCTTGGCTCC 180
 QY 181 CTTCCACATCCATGACGCCCAATGATCGGTGTACA 216
 DB 181 CTTCCACATCCATGACGCCCAATGATCGGTGTACA 216

RESULT 2
 BD155987 2123 bp DNA linear PAT 17-JAN-2003
 LOCUS
 DEFINITION
 Primer for synthesizing full-length cDNA and use thereof.
 ACCESSION
 BD155987 GI:27861745
 VERSION
 JP 2002191363-A/10830.
 KEYWORDS
 Homo sapiens (human)
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
 AUTHORS
 1 (bases 1 to 2123)
 Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
 Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
 TITLE
 Primer for synthesizing full-length cDNA and use thereof
 JOURNAL
 Patent: JP 2002191363-A 10830 09-JUL-2002;
 COMMENT
 HELIX RESEARCH INSTITUTE
 OS Homo sapiens (human)
 PN JP 2002191363-A/10830
 PD 09-JUL-2002
 PE 28-JUL-2000 JP 2000280990
 PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KOJI
 PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
 PI KEIICHI NAGAI,TETSUJI OTSUKI

PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/PC
 10,
 PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N5/00,C12N5/00 CC
 Primer for synthesizing full-length cDNA and use thereof FH Key
 FT CDS Location/Qualifiers
 (127)..(1647).

source

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 /db_xref="taxon:9606"
 BASE COUNT 550 a 664 c 528 g 381 t
 ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 8.4e-42;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCCGCCGCCGCCGAGAGGGTGACTCCATCCAGGTGCACAGCTCCAGCCATCTGGC 60
 DB 1432 CCGCCGCCGCCGCCGAGAGGGTGACTCCATCCAGGTGCACAGCTCCAGCCATCTGGC 1491
 QY 61 CAGGCCGTGACTGTCTCGAGGAGGAGCCGCTCAAGCGCTCAACCTCACTGACAGAGTGC 120
 DB 1492 CAGGCCGTGACTGTCTCGAGGAGGAGCCGCTCAAGCGCTCAACCTCACTGACAGAGTGC 1551
 QY 121 GGGCTGAAGCGTAGCGCCCTCGCTAAAGCGGAGAGTACCCCAACCAATCCTTGGCTCC 180
 DB 1552 GGGCTGAAGCGTAGCGCCCTCGCTAAAGCGGAGAGTACCCCAACCAATCCTTGGCTCC 1611
 QY 181 CTTCCACATCCATGACGCCCAATGATCGGTGTACA 216
 DB 1612 CTTCCACATCCATGACGCCCAATGATCGGTGTACA 1647

RESULT 3
 AK027439 2123 bp mRNA linear PRI 01-AUG-2002
 LOCUS
 DEFINITION
 Homo sapiens cDNA FLJ14533 fis, clone NT2RM2000407, moderately
 similar to Mus musculus semaphorin 1A mRNA.
 ACCESSION
 AK027439
 VERSION
 AK027439.1 GI:14042113
 KEYWORDS
 oligo capping; fis (full insert sequence).
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
 AUTHORS
 1
 Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
 Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H.,
 Wagatsuma,M., Hosoi,T., Kaku,Y., Kodaira,H., Kondo,H.,
 Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K.,
 Ono,Y., Takiyuchi,S., Watanabe,S., Kimura,K., Murakami,K.,
 Ishii,S., Kawai,Y., Saito,K., Yamamoto,D., Wakamatsu,A.,
 Nakamura,Y., Nagahara,K., Masuno,Y., Nimomiya,K. and Iwayanagi,T.
 TITLE
 NEDO human cDNA sequencing project
 JOURNAL
 Unpublished
 REFERENCE
 2 (bases 1 to 2123)
 Isogai,T. and Otsuki,T.
 DIRECT SUBMISSION

COMMENT
 Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
 Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 (E-mail:genomics@hri.co.jp Tel:81-438-52-3975, Fax:81-438-52-3986)
 NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing;
 Research Association for Biotechnology; cDNA library construction;
 5'-3'-end one pass sequencing and clone selection; Helix
 Research Institute (supported by Japan Key Technology Center etc.)
 and Department of Virology, Institute of Medical Science,
 University of Tokyo.

FEATURES
 source Location/Qualifiers

1..2123
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 /clone="NT2RM2000407"
 /cell_line="NT2"
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 /clone_1b="NT2RM2"
 /note="Cloning vector: pUC19FL3-mRNA from uninduced NT2

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        VORKEKETHSRRSGMSVYTKLSGIFGDQSKDPKPEALITPLMHNGKILATPGNTAKM
        LIRADQHHDLALPTPESTPTIQOKRKPRGSRERNONLINACTKMPPPGSPYI
        PTDLPLKASPSHLPSVYVLPITQOGYQHEVVDPKKSEVAKMLLEDQATLEKTIKE
        HLSSKSPNHGVNLVENIDSLPRVPOQEGASLSQGLSKRLMEMHSSSYGD
        YKRSYPTNSLTSRHOATTLKRNNTNSNSHLSRQSFGRDNDPAPQVRDYSIOVS
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BASE COUNT      550 a      664 c      528 g      381 t

ORIGIN
    Query Match      100.0%; Score 216; DB 9; Length 2123;
    Best Local Similarity 100.0%; Pred. No. 8.4e-42;
    Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCGCGCGCGCGCGCGAGAGGGTGAGTCCATCCAGSTGCACACGCTCCAGCCATCTGCG 60
DB      1432 CCGCGCGCGCGCGCGAGAGGGTGAGTCCATCCAGSTGCACACGCTCCAGCCATCTGCG 1491
QY      61 CAGGCGGTGACTGTCTCGAGGACAGCCAGCCTCAACGCTCAACTGCTGACAAGGTGC 120
DB      1492 CAGGCGGTGACTGTCTCGAGGACAGCCAGCCTCAACGCTCAACTGCTGACAAGGTGC 1551
QY      121 GGGCTGAAGCGTACGCCCTCGCTAAAGCGGAGCTACCCCCAAACCATCTTTGCTGCC 180
DB      1552 GGGCTGAAGCGTACGCCCTCGCTAAAGCGGAGCTACCCCCAAACCATCTTTGCTGCC 1611
QY      181 CTTTCACATCCATGAAAGCCCAATGAGCGGTGACA 216
DB      1612 CTTTCACATCCATGAAAGCCCAATGAGCGGTGACA 1647

RESULT 4
BD127394      2227 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION    Primer for synthesizing full-length cDNA and use thereof.
ACCESSION     BD127394.1 GI:23222339
VERSION       JP 2002017375-A/2825.
KEYWORDS
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
TITLE         Primer for synthesizing full-length cDNA and use thereof
JOURNAL       Patient: JP 2002017375-A 2825 22-JAN-2002;
COMMENT
HELIX RESEARCH INSTITUTE
OS      Homo sapiens (human)
PN      JP 2002017375-A/2825
PD      22-JAN-2002
PE      07-JUN-2000 JP 2000253172
PI      TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
PI      ISHII,
PI      YORI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI      TETSUO OTSUKI,HISASHI KOGA
PC      C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
10, PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
FT      CDS      Location/Qualifiers
(56)..(1741).

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FEATURES
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            /db_xref="taxon:9606"

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ORIGIN
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    Best Local Similarity 100.0%; Pred. No. 8.4e-42;
    Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCGCGCGCGCGCGCGAGAGGGTGAGTCCATCCAGSTGCACACGCTCCAGCCATCTGCG 60
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QY      61 CAGGCGGTGACTGTCTCGAGGACAGCCAGCCTCAACGCTCAACTGCTGACAAGGTGC 120
DB      1586 CAGGCGGTGACTGTCTCGAGGACAGCCAGCCTCAACGCTCAACTGCTGACAAGGTGC 1645
QY      121 GGGCTGAAGCGTACGCCCTCGCTAAAGCGGAGCTACCCCCAAACCATCTTTGCTGCC 180
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QY      181 CTTTCACATCCATGAAAGCCCAATGAGCGGTGACA 216
DB      1706 CTTTCACATCCATGAAAGCCCAATGAGCGGTGACA 1741

RESULT 5
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LOCUS         AK074975
DEFINITION    Homo sapiens cDNA FLJ90494 f1s, clone NT2RP3003614.
ACCESSION     AK074975
VERSION       AK074975.1 GI:22760768
KEYWORDS      oligo capping: f1s (full insert sequence).
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1
Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T.,
Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S.,
Kawai,Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y.,
Kojima,S., Nagahara,K., Masuo,Y., Ota,T., Okano,K., Yoshikawa,Y.,
Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and
Ninomiya,K.
TITLE         NEDO human cDNA sequencing project
JOURNAL       Unpublished
AUTHORS
REFERENCE     Direct Submission
TITLES        Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology; cDNA library construction:
Institute of Medical Science, University of Tokyo, laboratory of
Genome Structure, Human Genome Center; cDNA 5'-3' end one pass
sequencing and clone selection; Helix Research Institute (supported
by Japan Key Technology Center etc.).
LOCATION/Qualifiers
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/cell_type="teratocarcinoma"
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precursor cells after 2-weeks retinoic acid (RA)

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CDS

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DKKGVITRESYKGDOLVPTLLAIAVILAIFVGVAVSGITVVCYCDHRRRDVAVVR
KKEHLTISRSGMSVTKLSGLRDTQSKPKPEALITPLMHNKDLPENTAKMLIK
ADQHHLDLALPPESTPTLQQRKRPERSREWERNONLINACTKDPMPGSPVLPD
LPLRASSHLPVYVLEITQOQYQHEVVDQPKMSVQAQMLLEDQALLEYKTIKELHS
SKSPHGVNIVENLDSLPKVPQREASLGPKASLQGTGLSPKLEMHSSSYGVYKR
SYPNLSLTRSHQATTLTKRNTNSNSHLSRNOSEFGSDSPAPORVDSIOVSSQSP
SGQAVTYSRQSLNAYNSLTRNSGLKRPISLKPDPVPRPSPAPLSTSKRPADACT"

BASE COUNT 567 a 700 c 560 g 400 t

ORIGIN

Query Match 100.0%; Score 216; DB 9; Length 2227;
Best Local Similarity 100.0%; Pred. No. 8.4e-42;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCCGCCCGCCCGCAGAGGGGTGACTCCATCCAGGTGCACAGCTCCCAAGCATCTGGC 60
DB 1526 CCGCCGCCCGCCCGCAGAGGGGTGACTCCATCCAGGTGCACAGCTCCCAAGCATCTGGC 1585
QY 61 CAGGCGGTGACTGCTGTGAGGACAGCCAGCTCAGGCTCAAGCCTCAACATCAGTACAGGTCG 120
DB 1586 CAGGCGGTGACTGCTGTGAGGACAGCCAGCTCAGGCTCAAGCCTCAACATCAGTACAGGTCG 1645
QY 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCGGAGCTACCCCCCAACCATCTTGTCTGCC 180
DB 1646 GGGCTGAAGCGTACGCCCTCGCTAAAGCGGAGCTACCCCCCAACCATCTTGTCTGCC 1705
QY 1646 GGGCTGAAGCGTACGCCCTCGCTAAAGCGGAGCTACCCCCCAACCATCTTGTCTGCC 1705
DB 181 CTTTCCATCCATCAGAACCCCAATGATGCGGTGACA 216
QY 1706 CTTTCCATCCATCAGAACCCCAATGATGCGGTGACA 1741
DB 1706 CTTTCCATCCATCAGAACCCCAATGATGCGGTGACA 1741

RESULT 6
BD157826 2293 bp DNA linear PAT 17-JAN-2003
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BD157826 2293 bp DNA linear PAT 17-JAN-2003
BD157826 1 GI:27863584
JP 2002191363-A/12669.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2293)
Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002191363-A 12669 09-JUL-2002;
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002191363-A/12669
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORI
SAITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KEIICHI NAGAI, TETSUJI OTSUKI
PC
C12N15/09, C07K14/47, C07K16/18, C12N1/25, C12N1/19, C12N1/21, C12N5/ PC
10, C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
PC Primer for synthesizing full-length cDNA and use thereof PH Key
Location/Qualifiers
FT CDS (138)..(1823).
Location/Qualifiers

source

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BASE COUNT 579 a 713 c 581 g 420 t

ORIGIN

Query Match 100.0%; Score 216; DB 6; Length 2293;
Best Local Similarity 100.0%; Pred. No. 8.4e-42;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCCGCCCGCCCGCAGAGGGGTGACTCCATCCAGGTGCACAGCTCCCAAGCATCTGGC 60
DB 1608 CCGCCGCCCGCCCGCAGAGGGGTGACTCCATCCAGGTGCACAGCTCCCAAGCATCTGGC 1667
QY 61 CAGGCGGTGACTGCTGTGAGGACAGCCAGCTCAGGCTCAAGCCTCAACATCAGTACAGGTCG 120
DB 1668 CAGGCGGTGACTGCTGTGAGGACAGCCAGCTCAGGCTCAAGCCTCAACATCAGTACAGGTCG 1727
QY 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCGGAGCTACCCCCCAACCATCTTGTCTGCC 180
DB 1728 GGGCTGAAGCGTACGCCCTCGCTAAAGCGGAGCTACCCCCCAACCATCTTGTCTGCC 1787
QY 181 CTTTCCATCCATCAGAACCCCAATGATGCGGTGACA 216
DB 1788 CTTTCCATCCATCAGAACCCCAATGATGCGGTGACA 1823

RESULT 7
AK027471 2293 bp mRNA linear PRI 01-AUG-2002
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AK027471 2293 bp mRNA linear PRI 01-AUG-2002
AK027471
Homo sapiens cDNA FLJ14565 fis, clone NT2RM4000233, highly similar
to Mus musculus semaphorin 1A mRNA.
AK027471.1 GI:14042170
oligo capping, fis (full insert sequence).
Homo sapiens
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1
Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H.,
Wagatsuma,M., Hosohiri,T., Kaku,Y., Kodaira,H., Kondo,H.,
Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K.,
Oto,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K.,
Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,
Nakamura,Y., Nagahari,K., Masuo,Y., Niinomiya,K. and Iwayanagi,T.
NEBO human cDNA sequencing project
Unpublished
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

2 (bases 1 to 2293)
Isogai,T. and Otsuki,T.
Direct Submission
Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:01-438-52-3975, Fax:81-438-52-3986)
NEBO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing;
Research Association for Biotechnology; cDNA library construction,
5'-3' end one pass sequencing and clone selection; Helix
Research Institute (supported by Japan Key Technology Center etc.)
and Department of Virology, Institute of Medical Science,
University of Tokyo.
Location/Qualifiers
1..2293
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RM4000233"
/cell_line="NT2"
/cell_type="teratocarcinoma"
/clone_id="NT2RM4"
/note="Cloning vector: pUC19FL3-mRNA from uninduced NT2"

FEATURES
source

CDS

neuronal precursor cells."

138..1826

/note="unnamed protein product"

/codon_start=1

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/translation="MSVYNSERKSYDGEVDEKRMGMOLDRASSLTVAFSTCVIKVPL
GRCRRHGRCKKTKIASRDPYCGMTEKSGAGCHLSPNRSLTFEODIERKNDGLGDCIN
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DKKGVIRESSYLKGDQVPTVLAIAVLAIVKAVSGITVPCDHRKDVAVVOR
KEKELHSRRRSMSSVTKLGLFSDTQKDPKPEALITPLIMVNCVCDHRKDVAVVOR
ADQHLDTLALPPESTPTLOOKRKPSPGSEMERONLIMACTKMDPMGSPVPLPD
LPRASPSHDSVAVLPTIOGVOHEVVDOPKSEVOMALEQAAATLEKTEKHEHS
SKSPNHSVNLVENYDLSLPKYPKPREASLSPGASLSTGLSKRELMHSSSYGVYKR
SYFNSLIRSHQATTLTKRNNTSSNSHLSNOSFSGNDNPPAPKPVSDSIOVHSSDP
SGQAVVYSRQPSLAINYSLTRSLKRPISLKPDPKPPSPFAPLSTSMKPNDACT"

BASE COUNT 579 a 713 c 581 g 420 t

ORIGIN

Query Match 100.0%; Score 216; DB 9; Length 2293;
Best Local Similarity 100.0%; Pred. No. 8.4e-42;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCGCGCGCGCGCGAGAGGGTGGACTCCATCCAGTGCACAGCTCCACCATCTGGC 60
|||||
Db 1608 CCGCGCGCGCGCGCGAGAGGGTGGACTCCATCCAGTGCACAGCTCCACCATCTGGC 1667
|||||

QY 61 CAGGCGGTGACTGTCTCGAGGCGAGCCCAAGCCTCAAGCCTCAACTGACAGCAAGTGC 120
|||||
Db 1668 CAGGCGGTGACTGTCTCGAGGCGAGCCCAAGCCTCAAGCCTCAACTGACAGCAAGTGC 1727
|||||

QY 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCGGAGCGAGTACCCCCCAACCATCTTGGCTGCC 180
|||||
Db 1728 GGGCTGAAGCGTACGCCCTCGCTAAAGCGGAGCGAGTACCCCCCAACCATCTTGGCTGCC 1787
|||||

QY 181 CTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
|||||
Db 1788 CTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1823
|||||

RESULT 8
LOCUS BD159853 2306 bp DNA linear PAT 17-JAN-2003
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD159853
VERSION BD159853.1 GI:27865611
KEYWORDS JP 2002191363-A/14696.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2306)
Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002191363-A 14696 09-JUL-2002;
HELIX RESEARCH INSTITUTE

COMMENT
OS Homo sapiens (human)
PN JP 2002191363-A/14696
PD 09-JUL-2002
PI 28-JUL-2000 JP 2000280990
PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
PI SAITO,
PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
PI KEIICHI NAGAI,TETSUJI OTSUKI
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
10', C12P21/02,C12Q1/68//C12P21/08,G06F17/30 C12N15/00,C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH key
Location/Qualifiers
FT CDS Location/Qualifiers (109)..(1830).

FEATURES

source 1..2306

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

BASE COUNT 579 a 739 c 577 g 411 t

ORIGIN

Query Match 100.0%; Score 216; DB 6; Length 2306;
Best Local Similarity 100.0%; Pred. No. 8.3e-42;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCGCGCGCGCGCGAGAGGGTGGACTCCATCCAGTGCACAGCTCCACCATCTGGC 60
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Db 1615 CCGCGCGCGCGCGCGAGAGGGTGGACTCCATCCAGTGCACAGCTCCACCATCTGGC 1674
|||||

QY 61 CAGGCGGTGACTGTCTCGAGGCGAGCCCAAGCCTCAAGCCTCAACTGACAGCAAGTGC 120
|||||
Db 1675 CAGGCGGTGACTGTCTCGAGGCGAGCCCAAGCCTCAAGCCTCAACTGACAGCAAGTGC 1734
|||||

QY 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCGGAGCGAGTACCCCCCAACCATCTTGGCTGCC 180
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Db 1735 GGGCTGAAGCGTACGCCCTCGCTAAAGCGGAGCGAGTACCCCCCAACCATCTTGGCTGCC 1794
|||||

QY 181 CTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
|||||
Db 1795 CTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1830
|||||

RESULT 9
LOCUS AK027654 2306 bp mRNA linear PRI 01-AUG-2002
DEFINITION Homo sapiens cDNA FL14748 f1s, clone NT2R3002869, highly similar
to Mus musculus semaphorin 1A mRNA.
ACCESSION AK027654
VERSION AK027654.1 GI:14042491
KEYWORDS oligo capping; f1s (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2306)
Isogai,T. and Otsuki,T.
Direct Submission
Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert construction;
Research Association for Biotechnology; cDNA library construction;
5'-3' end one pass sequencing and clone selection; Helix
Research Institute (supported by Japan Key Technology Center etc.)
and Department of Virology, Institute of Medical Science,
University of Tokyo.
Location/Qualifiers
1..2306
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2R3002869"
/cell_line="NT2"
/cell_type="fibroblast carcinoma"
/clone_lib="NT2R3"
/note="Cloning vector: pME18Sf13-mRNA from NT2 neuronal

FEATURES

CDS

precursor cells after 2-weeks retinoic acid (RA)
induction."
109..1833
/note="unnamed protein product"
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DPLGAVSSHNDKRGVIRESTYLGHDQVLAVILAVILAEVMAVSEGTIVYCC
DHRKDAVAVQREKELTHSRGSMSSVTLSGIFGTQSKDPEALPLPMMNGTL
ATPNTAKMLIKADHDHDLTALPTPESTTLQKRPSPRSERERNOMIACD
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TLEKTKIKELSSKSPHGVNIVENLDSLEPKYPORASISPGASISQNGLSKRLM
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MKPNDACT"

BASE COUNT 579 a 739 c 577 g 411 t

Query Match 100.0%; Score 216; DB 9; Length 2306;
Best Local Similarity 100.0%; Pred. No. 8.3e-42;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCCGCGCCCGCCGAGAGGGTGGACTCCATCCAGGTGACACAGCTCCAGCCATCTGGC 60
|||||
Db 1615 CCGCCGCGCCCGCCGAGAGGGTGGACTCCATCCAGGTGACACAGCTCCAGCCATCTGGC 1674

QY 61 CAGGCCGTGACTGTCTCGAGGACAGCCAGCTCAAGCCTCAACACTGACAGAGTGC 120
|||||
Db 1675 CAGGCCGTGACTGTCTCGAGGACAGCCAGCTCAAGCCTCAACACTGACAGAGTGC 1734

QY 121 GGGCTGAAGGTAGCGCCCTGCTAAGCCGAGAGTACCCCAACCATCTTGTGCTGCC 180
|||||
Db 1735 GGGCTGAAGGTAGCGCCCTGCTAAGCCGAGAGTACCCCAACCATCTTGTGCTGCC 1794

QY 181 CTTTCACATCCATGAAGCCCAATGATGCGGTGACA 216
|||||
Db 1795 CTTTCACATCCATGAAGCCCAATGATGCGGTGACA 1830

RESULT 10
BD159617 3041 bp DNA linear PAT 17-JAN-2003
LOCUS BD159617
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD159617
VERSION BD159617.1 GI:27865375
KEYWORDS JP 2002191363-A/14460.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3041)
Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002191363-A 14460 09-JUL-2002;
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN 2002191363-A/14460
PD 09-JUL-2002
PE 28-JUL-2000 JP 2000280990
PI TOSHIO OTA,TAKAO ISOGAI,TEISUO NISHIKAWA,KOJI HAYASHI,KAORU
PI SAITO,
PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
PI KEIICHI NAGAI,TEISUJI OTSUKI
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/-9,C12N1/21,C12N5/ PC
10,
PC C12P21/02,C12P1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers

FEATURES FT CDS (85)..(2181).
Location/Qualifiers
1..3041
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 804 a 886 c 714 g 637 t

Query Match 100.0%; Score 216; DB 6; Length 3041;
Best Local Similarity 100.0%; Pred. No. 8e-42;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCCGCGCCCGCCGAGAGGGTGGACTCCATCCAGGTGACACAGCTCCAGCCATCTGGC 60
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Db 1966 CCGCCGCGCCCGCCGAGAGGGTGGACTCCATCCAGGTGACACAGCTCCAGCCATCTGGC 2025

QY 61 CAGGCCGTGACTGTCTCGAGGACAGCCAGCTCAAGCCTCAACACTGACAGAGTGC 120
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Db 2026 CAGGCCGTGACTGTCTCGAGGACAGCCAGCTCAAGCCTCAACACTGACAGAGTGC 2085

QY 121 GGGCTGAAGGTAGCGCCCTGCTAAGCCGAGAGTACCCCAACCATCTTGTGCTGCC 180
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Db 2086 GGGCTGAAGGTAGCGCCCTGCTAAGCCGAGAGTACCCCAACCATCTTGTGCTGCC 2145

QY 181 CTTTCACATCCATGAAGCCCAATGATGCGGTGACA 216
|||||
Db 2146 CTTTCACATCCATGAAGCCCAATGATGCGGTGACA 2181

RESULT 11
AK027501 3041 bp mRNA linear PRI 01-AUG-2002
LOCUS AK027501
DEFINITION Homo sapiens cDNA FLJ14595 fts, clone NT2RM4002194, highly similar
to Mus musculus semaphorin 7A mRNA.
ACCESSION AK027501
VERSION AK027501.1 GI:14042222
KEYWORDS clligo capping; fts (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H.,
Wagatsuma,M., Hosokawa,T., Kaku,Y., Kodaira,H., Kondo,H.,
Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K.,
Oto,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K.,
Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,
Nakamura,Y., Nagahata,K., Masuko,Y., Ninomiya,K. and Iwayanagi,I.
TITLE NEDO human cDNA sequencing project
JOURNAL NEDO human cDNA sequencing project
REFERENCE 2 (bases 1 to 3041)
Isogai,T. and Otsuki,T.
TITLE Direct Submission
JOURNAL Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 297-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing;
Research Association for Biotechnology; cDNA library construction;
5'-3'-end one pass sequencing and clone selection; Helix
Research Institute (supported by Japan Key Technology Center etc.)
and Department of Virology, Institute of Medical Science,
University of Tokyo.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RM4002194"
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/cell_type="teratocarcinoma"

CDS

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/note="cloning vector: pUC19FL3-mRNA from uninduced NT2
neuronal precursor cells."
85..2164
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/db_start=1

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LBRASSILVARSCTVYIKVGRCEHGRCKTCIASRDYCGWIKEGGACSLSPNS
RLTFEDIDTRGNTDGLDCHNSPVALNHSLSLPTSTDSQTAQEGYSGRMGLMK
HLSDSPDSTDPGAVASNNHODKCYTRSYSLKGHQLYPVLIAVLAIVMGAVF
SGITVYCVCDHRRKDYAVVORKEKELTHSRGSSSVTLISGLFGDQSDKPEAL
TPLMNGKLTAPGNTAKMLIKADHMLDLTALPPESTPTLQOKRPSRSGREMERNO
NLINACTKMPGSPVPIPTDLIRASPSHISVVLPTQOGYQHEHYDOPMERNO
OMALEDOATLEKTIKEHLSSKPNHGVNLVNLSPKVPQREASLGPASLSQ
GLSKREHHSNHSVGVDYKRSYPTNSLTRSHQATTLKRNNTNSNSHLSRQSFGR
GDNPPAPRQVDSIOYHSSQPSQANTVSRQPSLNNVNSLTRGLKRTSLKRDVPRK
PSFAPLSTSMKPDACT"

BASE COUNT 804 a 886 c 714 g 637 t
ORIGIN

Query Match 100.0%; Score 216; DB 9; Length 3041;
Best Local Similarity 100.0%; Pred. No. 8e-42;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCCGCCGCCCGCCGAGAGGGTGAGTCCATCCAGGTGCACAGCTCCAGCCATCTGGC 60
|||||
Db 1966 CCGCCGCCGCCCGCCGAGAGGGTGAGTCCATCCAGGTGCACAGCTCCAGCCATCTGGC 2025
QY 61 CAGGCGCTGACTGTCTCGAGGACAGCCAGCTTCAAGCCTTCAACTACTGACAAAGTGC 120
|||||
Db 2026 CAGGCGCTGACTGTCTCGAGGACAGCCAGCTTCAAGCCTTCAACTACTGACAAAGTGC 2085
QY 121 GGGCTGAAGGCTAGCGCCCTGCTAAAGCGGAGCTACCCGCCAACCATTCTTGTGCTCC 180
|||||
Db 2086 GGGCTGAAGGCTAGCGCCCTGCTAAAGCGGAGCTACCCGCCAACCATTCTTGTGCTCC 2145
QY 181 CTTTCACATCCATGAAGCCCAATGATGCGTGTACA 216
|||||
Db 2146 CTTTCACATCCATGAAGCCCAATGATGCGTGTACA 2181

RESULT 12
AX026741 3093 bp DNA linear PAT 16-SEP-2000
LOCUS
DEFINITION Sequence 1 from Patent WO0031252.
ACCESSION AX026741
VERSION AX026741.1 GI:10187886
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1
TITLE Klostermann, A. and Behl, C.
JOURNAL Human semaphorin 6a-1 (sema6a-a), a gene involved in neuronal
development and regeneration mechanisms during apoptosis, and its
use as a potential drug target
Patent: WO 0031252-A 1 02-JUN-2000;
KLOSTERMANN ANDREAS (DE); MAX PLANCK GESELLSCHAFT (DE); BEHL
CHRISTIAN (DE)
FEATURES
source location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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/db_xref="GI:10187887"

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EPYFQAVDYGDIYFFREIAVEYNTMKVPRVAQYCKNDGSGORYLEKQWTF
LKARLNCVSGDSHEFTYFNLQADTVIRNGROVLAFTSPNYSIPGSAVAYMDID
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KTHPLMDEAVPSIFNRPWFLRTMVRRLTKIADTAAGPYQNTVPLISGKGIILKE
LNTGSGFLNLSLEEMSYNSEKSYDYGEDKIMQDLRSDSPDSTDPGAVAS
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CHNSPVALNHSLSLPTSTDSQTAQEGYSGRMGLHLDSPDSTDPGAVAS
HNHODKGYTRSYSLKGHQLYPVLIAVLAIVMGAVFSGITVYCVCDHRRKDYA
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IPDLIRASPSHISVVLPTQOGYQHEHYDOPMERNOOMALEDOATLEKTIKE
HLSSKPNHGVNLVNLSPKVPQREASLGPASLSQGLSKREHHSNHSVGVDYKRSY
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BASE COUNT 813 a 855 c 765 g 660 t
ORIGIN

Query Match 100.0%; Score 216; DB 6; Length 3093;
Best Local Similarity 100.0%; Pred. No. 8e-42;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCCGCCGCCCGCCGAGAGGGTGAGTCCATCCAGGTGCACAGCTCCAGCCATCTGGC 60
|||||
Db 2875 CCGCCGCCGCCCGCCGAGAGGGTGAGTCCATCCAGGTGCACAGCTCCAGCCATCTGGC 2934
QY 61 CAGGCGCTGACTGTCTCGAGGACAGCCAGCTTCAAGCCTTCAACTACTGACAAAGTGC 120
|||||
Db 2935 CAGGCGCTGACTGTCTCGAGGACAGCCAGCTTCAAGCCTTCAACTACTGACAAAGTGC 2994
QY 121 GGGCTGAAGGCTAGCGCCCTGCTAAAGCGGAGCTACCCGCCAACCATTCTTGTGCTCC 180
|||||
Db 2995 GGGCTGAAGGCTAGCGCCCTGCTAAAGCGGAGCTACCCGCCAACCATTCTTGTGCTCC 3054
QY 181 CTTTCACATCCATGAAGCCCAATGATGCGTGTACA 216
|||||
Db 3055 CTTTCACATCCATGAAGCCCAATGATGCGTGTACA 3090

RESULT 13
AX099520 3550 bp DNA linear PAT 02-APR-2001
LOCUS
DEFINITION Sequence 160 from Patent WO0119988.
ACCESSION AX099520
VERSION AX099520.1 GI:13538594
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1
TITLE Jacobs, K., McCoy, J.M., Lavallie, E.R., Collins-Racie, L.A., Evans, C.,
Merberg, D., Treacy, M., Bowman, M.R., Spaulding, V. and Agostino, M.J.
JOURNAL Secreted proteins and polynucleotides encoding them
Patent: WO 0119988-A 160 22-MAR-2001;
Genetics Institute, Inc. (US)
FEATURES
source location/Qualifiers
1..3550
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
1..3550
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/codon_start=1
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BASE COUNT 957 a 994 c 856 g 742 t 1 others
ORIGIN

Query Match 100.0%; Score 216; DB 6; Length 3550;
Best Local Similarity 100.0%; Pred. No. 7.9e-42;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCGCCGCGCCCGGAGAGGTGGAGTCCATCCAGGTGACAGCTCCAGCCATCTGGC 60
 |||
 Db 2835 CCGCGCCGCGCCCGGAGAGGTGGAGTCCATCCAGGTGACAGCTCCAGCCATCTGGC 2884
 |||
 QY 61 CAGCGCGTGAAGTCTCTGAGAGGAGCCAGCCCTCAACGCTACAACTCACTGACAGGTGC 120
 |||
 Db 2895 CAGCGCGTGAAGTCTCTGAGAGGAGCCAGCCCTCAACGCTACAACTCACTGACAGGTGC 2954
 |||
 QY 121 GGGCTGAAGGTACGCGCTCTGCTAAAGCCGAGCTACCCCGCAACCATCTTTGCTGCC 180
 |||
 Db 2955 GGGCTGAAGGTACGCGCTCTGCTAAAGCCGAGCTACCCCGCAACCATCTTTGCTGCC 3014
 |||
 QY 181 CTTTCACATCATGAGAGCCCAATGATGCGGTACA 216
 |||
 Db 3015 CTTTCACATCATGAGAGCCCAATGATGCGGTACA 3050
 |||

RESULT 14

AK096337

LOCUS AK096337 3634 bp mRNA linear PRI 15-JUL-2002
 DEFINITION Homo sapiens cDNA FLJ39018 fis, clone NT2RP7002594, highly similar
 to Homo sapiens semaphorin SEMA6A mRNA.

ACCESSION

AK096337

VERSION

AK096337.1 GI:21755807

KEYWORDS

oligo capping; fis (full insert sequence).

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS

1 Niomiyu, K., Magatsuma, M., Kanda, K., Kondo, H., Yokoi, T.,
 Kodaira, H., Kutsu, T., Takahashi, M., Kikkawa, E., Omura, Y., Abe, K.,
 Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M.,
 Sugiyama, T., Ito, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S.,
 Yamamoto, J., Isono, Y., Kawai, H., Saito, K., Nishikawa, T.,
 Kimura, K., Yamashita, H., Matsuo, K., Nakamura, T., Sekine, M.,
 Kiuchi, H., Murakawa, K., Kawaguchi, K., Takahashi, T., Sugano, S.,
 Ohtsuka, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Nagai, K., and
 Isogai, T.

TITLE

NEDO human cDNA sequencing project

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 3634)

AUTHORS

Isogai, T. and Yamamoto, J.

TITLE

Direct Submission

JOURNAL

Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
 (E-mail: genomics@hri.co.jp, Tel. 81-438-52-3975, Fax: 81-438-52-3986)

COMMENT

NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:
 Research Association for Biotechnology (RAB); cDNA library
 construction: Helix Research Institute (HRI) (supported by Japan
 Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
 HRI, and Biotechnology Center, National Institute of Technology and
 Evaluation; clone selection for full insert sequencing: HRI and
 RAB; annotation: HRI and RAB.

FEATURES

Location/Qualifiers

1..3634

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="NT2RP7002594"

/cell_line="NT2"

/cell_type="teratocarcinoma"

/note="cloning vector: PMEL18FL3-mRNA from NT2 neuronal
 precursor cells after 5-weeks retinoic acid (RA)
 induction."

BASE COUNT

990 a 1014 c 805 g 825 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 216; DB 9; Length 3634;

Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCGCCGCGCCCGGAGAGGTGGAGTCCATCCAGGTGACAGCTCCAGCCATCTGGC 60
 |||
 Db 2943 CCGCGCCGCGCCCGGAGAGGTGGAGTCCATCCAGGTGACAGCTCCAGCCATCTGGC 3002
 |||
 QY 61 CAGCGCGTGAAGTCTCTGAGAGGAGCCAGCCCTCAACGCTACAACTCACTGACAGGTGC 120
 |||
 Db 3003 CAGCGCGTGAAGTCTCTGAGAGGAGCCAGCCCTCAACGCTACAACTCACTGACAGGTGC 3062
 |||
 QY 121 GGGCTGAAGGTACGCGCTCTGCTAAAGCCGAGCTACCCCGCAACCATCTTTGCTGCC 180
 |||
 Db 3063 GGGCTGAAGGTACGCGCTCTGCTAAAGCCGAGCTACCCCGCAACCATCTTTGCTGCC 3122
 |||
 QY 181 CTTTCACATCATGAGAGCCCAATGATGCGGTACA 216
 |||
 Db 3123 CTTTCACATCATGAGAGCCCAATGATGCGGTACA 3158
 |||

RESULT 15

AX026746

LOCUS AX026746 3862 bp DNA linear PAT 16-SEP-2000
 DEFINITION Sequence 6 from Patent WO0031252.

ACCESSION

AX026746

VERSION

AX026746.1 GI:10187890

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS

1 Klostermann, A. and Behl, C.

TITLE

Human semaphorin 6a-1 (sema6a-a), a gene involved in neuronal
 development and regeneration mechanisms during apoptosis, and its
 use as a potential drug target

JOURNAL

Patent: WO 0031252-A 6 02-JUN-2000;

KLOSTERMANN ANDREAS (DE); MAX PLANCK GESELLSCHAFT (DE); BEHL
 CHRISTIAN (DE)

FEATURES

Location/Qualifiers

1..3862

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

658..3750

/note="unnamed protein product"

/protein_id="CA09109.1"

/db_xref="GI:10187891"

/translation="MRSFALLLYFTLHFAAGPDESEPISSHNTYKQPVFVGH
 KPGNTTORHHDIDIMIMGTLTYAARDIIVVDISTHEEYCSKLTWKSROA
 DVTGCRKRGKDKCHNFITKILKKNDALPVCGTNNFPCRNKMTLEPGEDES
 GMARCPYDAKAAVALRDRGLYSAITVDLADAVIYRSGESPILRYVHDSKMTK
 EPRVQAVDYGDIYFFREIAYENVNGKVPFRAVQVCKNDGSGSVILEKWTSE
 LKARLNSVPDSDSEFFNYLQAVDVIRINRDVLAIFSTPYSIPQSAVCAVDMLD
 IASVTEGFEKQSPDSTWTVPDEYRIRKPPGCCAGSSSEIRATSEFPDQILNFI
 KTHPLMEAVPSINPWFELTWRVRLTAVTIAAPYVGNHVVFEYSKGIILKE
 LARLNGSEFLNDISLFIEMSVYNSKESYDKVEKRIKGMOLDRASSLYAFSCVI
 KVLGRDREKCKTKTASRDPTCGWIKREGACSHLSPNSRLTFEEDIEGNDGIG
 DHHNSFVALNGSSSLPSTSDTAGESESGKMDKMLHLDSPDTPICAVSS
 HNHDOKGVIRESYLKGDQVPTLALAVIALVMAVPSGLITVCCHRRKQDA
 VVORKEKELISRGSSSVTLKGLFEDTOSKPEPAITLPLMHNKLTPGTAK
 MLIKADHDLTLALPPESTPTLOOKRPPSGSEWRNOLINACKIDMPMGSPV
 IPTDILPASRPSVYVILITGOOGYHEVDOPKMEVOMALEDOATILEYTKG
 EHLSPKSNBYNLYENTDISLPRPYROEASLPGASLTGSGLSKRLTMMHSSSYG
 DYKRSYPTNSLTRSHOATTLKRNNTSSNSHLSFNQSFQGDNDPPAPAPVDSTQVH
 SSOPSGQAVTVSROPISLNAVNSLTRSGIKRTPSLKPDVPRFAPLSTSMKPNDACT
 "

BASE COUNT

971 a 1111 c 967 g 813 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 216; DB 6; Length 3862;

Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```
QY      1 CCGCCGCCCCCCCCGAGAGGGTGGACTCCATCCAGTGCACAGCTCCGAGCCATCTGGC 60
      |||||||
Db      3532 CCGCCGCCCCCCCCGAGAGGGTGGACTCCATCCAGTGCACAGCTCCGAGCCATCTGGC 3591
      |||||||
QY      61 CAGGCCGTGACTGTCTCGAGGAGGCCAGCTCAACGCTTACACTCACTGACAAGTGG 120
      |||||||
Db      3592 CAGGCCGTGACTGTCTCGAGGAGGCCAGCTTCAAGGCTTACACTCACTGACAAGTGG 3651
      |||||||
QY      121 GGGCTGAAAGCGTACGGCCCTCGCTAAAGCGGAGGTACCCCCCAAAACCATCTTTGCTGCC 180
      |||||||
Db      3652 GGGCTGAAAGCGTACGGCCCTCGCTAAAGCGGAGGTACCCCCCAAAACCATCTTTGCTGCC 3711
      |||||||
QY      181 CTTTCACATCCATGAAGCCCAATGATGGGTGACA 216
      |||||||
Db      3712 CTTTCACATCCATGAAGCCCAATGATGGGTGACA 3747
      |||||||
```

Search completed: September 30, 2003, 20:16:11
Job time : 775.266 secs

PF 26-NOV-1999; 99WO-EP09215.
 XX 26-NOV-1998; 98EP-0122441.
 XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX Behl C, Klostermann A;
 XX WPI: 2000-400065/34.
 DR P-PSDB: AAY71461.
 XX Nucleic acid coding for human semaphorin 6A-1 used as diagnostic agent,
 PT therapeutic agent, for modulating immune system, in gene therapy or for
 PT effecting differentiation, cytoskeletal stabilization and/or plasticity
 PT
 XX
 XX
 PS Claim 2; Page 21; 53pp; English.
 CC The present sequence is a DNA encoding binding domain of transmembranous
 CC human semaphorin 6A-1 (HSA)SEMA6A-1) which is involved in neuronal
 CC development and regeneration mechanisms during apoptosis. The binding
 CC domain shows homology to Zyxin protein and selectively binds to members
 CC of Ena/VASP protein family, especially Evi. (HSA)SEMA6A-1 is a
 CC member of protein family displaying secreted or transmembrane-based
 CC repulsive guidance cues critically involved in neuronal development.
 CC Expression of (HSA)SEMA6A-1 is highest in embryonic brain and
 CC kidney and moderate in lung. The present sequence is useful as diagnostic
 CC and therapeutic agents, for modulating the immune system, in gene
 CC therapy, for effecting differentiation, cytoskeletal stabilization
 CC and plasticity.
 XX
 XX
 SQ Sequence 216 BP; 45 A; 85 C; 51 G; 35 T; 0 other;
 Query Match 100.0%; Score 216; DB 21; Length 216;
 Best Local Similarity 100.0%; Pred. No. 2e-52;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCGCGCGCGCGCGCGAGGGGTGACTCCATCCAGGCGACAGTCCCGACCATCTGGC 60
 DB 1 CCGCGCGCGCGCGCGAGGGGTGACTCCATCCAGGCGACAGTCCCGACCATCTGGC 60
 QY 61 CAGGCGGTGACTGTCTCGAGGCGAGCCGAGCCTCAACGGCTACACTGACAGAGGTGC 120
 DB 61 CAGGCGGTGACTGTCTCGAGGCGAGCCGAGCCTCAACGGCTACACTGACAGAGGTGC 120
 QY 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCGCGAGCGACGATCCCGCAACCATCTTGTCTCC 180
 DB 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCGCGAGCGATCCCGCAACCATCTTGTCTCC 180
 QY 181 CTTTCACATCCATGAAGCCCAATGATGCTGTACA 216
 DB 181 CTTTCACATCCATGAAGCCCAATGATGCTGTACA 216
 RESULT 2
 AAC98050
 ID AAC98050 standard; cDNA; 1472 BP.
 XX AAC98050;
 AC
 XX
 XX 09-MAR-2001 (first entry)
 DE Human colon cancer antigen nucleotide sequence SEQ ID NO:60.
 XX
 XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW Identification; cytostatic; cardioactive; neuroprotective; vulnery;
 KW immunomodulatory; muscular; gynaecological; gastrointestinal;
 KW nephroprotective; antiinfective; antibacterial; gene therapy; wound;
 KW neural disorder; immune system disorder; muscular disorder;
 KW reproductive disorder; gastrointestinal disorder; renal disorder;
 KW infectious disease; cardiovascular disorder; ss.
 XX
 XX Homo sapiens.

XX
 XX W0200055351-A1.
 XX 21-SEP-2000.
 PD
 XX 08-MAR-2000; 2000WO-US05883.
 PF
 XX 12-MAR-1999; 99US-0124270.
 PR
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Rosen CA, Ruben SM;
 PI
 XX WPI: 2000-587534/55.
 DR P-PSDB: AAB53293.
 XX
 XX Colon cancer associated gene sequences, referred to as colon cancer
 PT antigens, useful for the treatment, prevention, and diagnosis of colon
 PT disorders such as colon cancer
 PT
 XX
 XX
 PS Claim 1; Page 510-511; 2104pp; English.
 CC AAC97991 to AAC98763 encode the human colon cancer associated proteins,
 CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
 CC human colon cancer antigens can have cytostatic, cardioactive, muscular;
 CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
 CC vulnery, nephroprotective, antiinfective and antibacterial activities, and
 CC can be used in gene therapy. The colon cancer antigen polynucleotides,
 CC proteins and antibodies for the proteins are useful for the prevention,
 CC treatment and diagnosis of colon disorders, such as colon cancer. The
 CC polynucleotides may be used in diagnostics and research, such as for
 CC chromosome identification, and as hybridisation probes. The proteins
 CC may also be used to prevent diseases such as neural disorders, immune
 CC system disorders, muscular disorders, reproductive disorders,
 CC gastrointestinal disorders, wounds, renal disorders, infectious
 CC diseases, and cardiovascular disorders. AAC98764 to AAC98772 and
 CC AAB54007 represent sequences used in the exemplification of the present
 CC invention.
 XX
 XX
 SQ Sequence 1472 BP; 437 A; 431 C; 299 G; 301 T; 4 other;
 Query Match 100.0%; Score 216; DB 21; Length 1472;
 Best Local Similarity 100.0%; Pred. No. 3.2e-52;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCGCGCGCGCGCGCGAGGGGTGACTCCATCCAGGCGACAGTCCCGACCATCTGGC 60
 DB 372 CCGCGCGCGCGCGCGAGGGGTGACTCCATCCAGGCGACAGTCCCGACCATCTGGC 431
 QY 61 CAGGCGGTGACTGTCTCGAGGCGAGCCGAGCCTCAACGGCTACACTGACAGAGGTGC 120
 DB 432 CAGGCGGTGACTGTCTCGAGGCGAGCCGAGCCTCAACGGCTACACTGACAGAGGTGC 491
 QY 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCGCGAGCGATCCCGCAACCATCTTGTCTCC 180
 DB 492 GGGCTGAAGCGTACGCCCTCGCTAAAGCGCGAGCGATCCCGCAACCATCTTGTCTCC 551
 QY 181 CTTTCACATCCATGAAGCCCAATGATGCTGTACA 216
 DB 552 CTTTCACATCCATGAAGCCCAATGATGCTGTACA 587
 RESULT 3
 AAH13995
 ID AAH13995 standard; cDNA; 2123 BP.
 XX AAH13995;
 AC
 XX 26-JUN-2001 (first entry)
 DE Human cDNA sequence SEQ ID NO:11072.
 XX
 XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 KW

XX Homo sapiens.
 OS
 XX EPI074617-A2.
 PN
 XX
 PD 07-FEB-2001.
 XX
 PF 28-JUL-2000; 2000EP-0116126.
 XX
 PR 29-JUL-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-0300253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX
 DR WPI; 2001-318749/34.
 XX
 PT Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length CDNA defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length CDNA.
 XX
 PS Claim 8; SEQ ID 11072; 2537pp + CD ROM; English.
 XX
 CC The present invention describes primer sets for synthesizing 5602
 CC full-length CDNA defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length CDNA. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length CDNA. The primers allow obtaining of the full-length
 CC CDNA easily without any specialized methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human CDNA sequences; AAH92446 to
 CC AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 XX
 SQ Sequence 2123 BP; 550 A; 664 C; 528 G; 381 T; 0 other.
 XX
 Query Match 100.0%; Score 216; DB 22; Length 2123;
 Best Local Similarity 100.0%; Pred. No. 3.5e-52;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCGCGCGCGCGCGAGAGGGTGGACTCCATCCAGTGCACAGCTCCCGAGCCATCTGGC 60
 DB 1432 CCGCGCGCGCGCGCGAGAGGGTGGACTCCATCCAGTGCACAGCTCCCGAGCCATCTGGC 1491
 QY 61 CAGGCGGTGACTGTCTCGAGGCGAGCCGCTCAACGCTCACTACTGACAAAGGTG 120
 DB 1492 CAGGCGGTGACTGTCTCGAGGCGAGCCGCTCAACGCTCACTACTGACAAAGGTG 1551
 QY 121 GGGCTGAAGCGTACGCGCTCGCTAAAGCGGAGCGTACCCCAACCAATCTTGTCTCC 180
 DB 1552 GGGCTGAAGCGTACGCGCTCGCTAAAGCGGAGCGTACCCCAACCAATCTTGTCTCC 1611
 QY 181 CTTTCCACATCCATGAAGCCCAATGATGCGGTACA 216
 DB 1612 CTTTCCACATCCATGAAGCCCAATGATGCGGTACA 1647

RESULT 4
 ID AAK94365
 XX AAK94365 standard; CDNA; 2227 BP.
 XX
 AC AAK94365;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human full-length CDNA, SEQ ID NO: 3087.
 XX
 KW Human; full length CDNA; CDNA synthesis; oligo-capping; ss.
 XX
 OS Homo sapiens.
 XX
 PN EPI130094-A2.
 XX
 PD 05-SEP-2001.
 XX
 PF 07-JUL-2000; 2000EP-0114089.
 XX
 PR 08-JUL-1999; 99JP-0194486.
 PR 11-JAN-2000; 2000JP-0118774.
 PR 02-MAY-2000; 2000JP-0183765.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX
 DR WPI; 2001-524255/58.
 DR P-PSDB; AAM93444.
 XX
 PT 830 Primers useful for synthesizing full length CDNA clones and their
 PT use in genetic manipulation -
 XX
 PS Claim 8; SEQ ID NO 3087; 1380pp + sequence listing; English.
 XX
 CC The invention relates to primers for synthesizing full length CDNA
 CC clones. 830 CDNA molecules encoding a human protein have been
 CC isolated and nucleotide sequences of 5'- and 3'-ends of the CDNA
 CC molecules have been determined. Primers for synthesizing the full length
 CC CDNA are useful for clarifying the function of the protein encoded by
 CC the CDNA. The full length clones were obtained by construction of full
 CC length enriched CDNA libraries that were synthesised by the oligo-capping
 CC method. The primers enable the production of the full length CDNA easily
 CC without any special methods. The present sequence is a full length
 CC human CDNA of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in CD-ROM format directly from EPO.
 XX
 SQ Sequence 2227 BP; 567 A; 700 C; 560 G; 400 T; 0 other;
 XX
 Query Match 100.0%; Score 216; DB 22; Length 2227;
 Best Local Similarity 100.0%; Pred. No. 3.6e-52;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCGCGCGCGCGCGAGAGGGTGGACTCCATCCAGTGCACAGCTCCCGAGCCATCTGGC 60
 DB 1526 CCGCGCGCGCGCGCGAGAGGGTGGACTCCATCCAGTGCACAGCTCCCGAGCCATCTGGC 1585
 QY 61 CAGGCGGTGACTGTCTCGAGGCGAGCCGCTCAACGCTCACTACTGACAAAGGTG 120
 DB 1586 CAGGCGGTGACTGTCTCGAGGCGAGCCGCTCAACGCTCACTACTGACAAAGGTG 1645
 QY 121 GGGCTGAAGCGTACGCGCTCGCTAAAGCGGAGCGTACCCCAACCAATCTTGTCTCC 180
 DB 1646 GGGCTGAAGCGTACGCGCTCGCTAAAGCGGAGCGTACCCCAACCAATCTTGTCTCC 1705
 QY 181 CTTTCCACATCCATGAAGCCCAATGATGCGGTACA 216
 DB 1706 CTTTCCACATCCATGAAGCCCAATGATGCGGTACA 1741

RESULT 5
ABK34739
ID ABK34739 standard; cDNA: 2262 BP.
XX
AC ABK34739;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human cDNA for novel secreted protein, SEQ ID 508.
XX
KW Human; ss: gene; secreted protein; immune deficiency; viral infection;
KW bacterial infection; fungal infection; autoimmune disorder; burn;
KW rheumatoid arthritis; multiple sclerosis; autoimmune thyroiditis;
KW diabetes; allergy; asthma; neurodegenerative disease; Crohn's disease;
KW Alzheimer's disease; Parkinson's disease; liver fibrosis; tumour;
KW coagulation disorder; haemophilia; inflammatory disorder; ulcer;
KW tissue regeneration; wound healing; haematopoiesis; myeloid deficiency;
KW lymphoid cell deficiency.
XX
OS Homo sapiens.
XX
PN WO200177290-A2.
XX
PD 18-OCT-2001.
XX
PF 29-MAR-2001; 2001WO-US10295.
XX
PR 06-APR-2000; 2000US-194941P.
XX
PA (GENEY) GENETICS INST INC.
XX
PI Wong GG, Clark HF, Fectel K, Agostino MJ, Howes SH, Resnick RJ;
PI Gulukota K, Graham JR;
XX
DR WPI: 2002-179323/23.
XX
PT Six hundred and twenty five polynucleotides derived from a variety of
PT human tissue sources which encode secreted proteins, useful for
PT treating immune deficiencies and disorders such as autoimmune disorders
XX
PS Claim 1; Page 272; 339pp; English.
XX
CC The invention relates to 625 polynucleotides which have been derived from
CC a variety of human tissue sources and which encode novel secreted
CC proteins, their complements and sequences that hybridise to them.
CC Also included are a vector comprising the polynucleotide, a host cell
CC transformed with the vector, the proteins encoded by the
CC polynucleotides, antibodies that bind to the proteins and identification
CC of modulators of the proteins or the expression of the polynucleotide.
CC The polynucleotides can be used as probes for the identification
CC and isolation of full length cDNA and genomic DNA. The polynucleotides
CC and proteins can also be used as nutritional supplements. The protein
CC is useful in the treatment of various immune deficiencies and disorders
CC such as viral infections, bacterial infections, fungal infections,
CC autoimmune disorders (e.g. rheumatoid arthritis, multiple sclerosis,
CC autoimmune thyroiditis and diabetes) and allergic reactions and
CC conditions (e.g. asthma). They are also useful for treating
CC neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's
CC disease), liver fibrosis, coagulation disorders (e.g. haemophilia),
CC inflammatory disorders (e.g. Crohn's disease) and tumours. They are also
CC useful for tissue regeneration, for wound healing and in the treatment
CC of burns, incisions and ulcers. The proteins are also useful for
CC regulating haematopoiesis, for treating myeloid or lymphoid cell
CC deficiencies. The present sequence is one of the 625 cDNA sequences
CC encoding a secreted protein.
XX
SQ Sequence 2262 BP; 604 A; 695 C; 522 G; 441 T; 0 other;

Query Match 100.0%; Score 216; DB 24; Length 2262;
Best Local Similarity 100.0%; Pred. No. 3.6e-52;

Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCGCCGCCCGCCCGCAGAGGGGTGACTCCATCCAGTGCACAGCTCCACCATTGCG 60
DB 1184 CCGCCGCCCGCCCGCAGAGGGGTGACTCCATCCAGTGCACAGCTCCACCATTGCG 1243
QY 61 CAGGCCGTGACTGCTCGAGGACGCCCTCAAGCGCTCAAGCGCTCAAGCGCTCAAGCGCTCG 120
DB 1244 CAGGCCGTGACTGCTCGAGGACGCCCTCAAGCGCTCAAGCGCTCAAGCGCTCG 1303
QY 121 GGGCTGAAGCGTACGCCCTCCCTAAAGCGGACGTACCCCAACCAATCCCTTTCCTCC 180
DB 1304 GGGCTGAAGCGTACGCCCTCCCTAAAGCGGACGTACCCCAACCAATCCCTTTCCTCC 1363
QY 181 CTTTCACATCCATGACGAGCCCAAGATGCTGTGACA 216
DB 1364 CTTTCACATCCATGACGAGCCCAAGATGCTGTGACA 1399
RESULT 6
AAH15834
ID AAH15834 standard; cDNA: 2293 BP.
XX
AC AAH15834;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:14327.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PI 07-FEB-2001.
XX
DR 28-JUL-2000; 2000EP-0116126.
XX
PF 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI: 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
PS Claim 8; SEQ ID 14327; 2537pp + CD ROM; English.
XX
CC The present invention describes primer sets for synthesizing 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,

CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to
 CC AAH58933 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.

XX Sequence 2293 BP; 579 A; 713 C; 581 G; 420 T; 0 other;

Query Match 100.0%; Score 216; DB 22; Length 2293;
 Best Local Similarity 100.0%; Pred. No. 3.6e-52;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCCGCCGCCGCCGAGAGGTGAGTCCATCCAGTGCACAGTCCAGCCATCTGGC 60
 DB 1608 CCGCCGCCGCCGCCGAGAGGTGAGTCCATCCAGTGCACAGTCCAGCCATCTGGC 1667
 QY 61 CAGGCCGTGACTGTCTCGAGGCGAGCCCAAGCTCAAGTCACTCACTGACAGAGTGC 120
 DB 1668 CAGGCCGTGACTGTCTCGAGGCGAGCCCAAGCTCAAGTCACTCACTGACAGAGTGC 1727
 QY 121 GGGCTGAAGCGTACGCCCTTCGCTAAGCGGAGCTACGCCCAACCATCTCTGCTGCC 180
 DB 1728 GGGCTGAAGCGTACGCCCTTCGCTAAGCGGAGCTACGCCCAACCATCTCTGCTGCC 1787
 QY 181 CTTTCACATCCATGAGCCCAATGATGCTGTGTACA 216
 DB 1788 CTTTCACATCCATGAGCCCAATGATGCTGTGTACA 1823

RESULT 7
 ID AAH17861 standard; cDNA; 2306 BP.

XX AAH17861;

DT 26-JUN-2001 (first entry)

DE Human cDNA sequence SEQ ID NO:17567.

XX Human; primer: detection; diagnosis; antisense therapy; gene therapy; ss.

OS Homo sapiens.

PN EP1074617-A2.

XX 07-FEB-2001.

PF 28-JUL-2000; 2000EP-0116126.

PR 29-JUL-1999; 99JP-0248036.

PR 27-AUG-1999; 99JP-0300253.

PR 11-JAN-2000; 2000JP-0118776.

PR 02-MAY-2000; 2000JP-0183767.

PR 09-JUN-2000; 2000JP-0241899.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI; 2001-318749/34.

PS Claim 8; SEQ ID 17567; 2537bp + CD ROM; English.

XX The present invention describes primer sets for synthesizing 5602

CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the combination of
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to
 CC AAH58933 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.

XX Sequence 2306 BP; 579 A; 739 C; 577 G; 411 T; 0 other;

Query Match 100.0%; Score 216; DB 22; Length 2306;
 Best Local Similarity 100.0%; Pred. No. 3.6e-52;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCCGCCGCCGCCGAGAGGTGAGTCCATCCAGTGCACAGTCCAGCCATCTGGC 60
 DB 1615 CCGCCGCCGCCGCCGAGAGGTGAGTCCATCCAGTGCACAGTCCAGCCATCTGGC 1674
 QY 61 CAGGCCGTGACTGTCTCGAGGCGAGCCCAAGCTCAAGTCACTCACTGACAGAGTGC 120
 DB 1675 CAGGCCGTGACTGTCTCGAGGCGAGCCCAAGCTCAAGTCACTCACTGACAGAGTGC 1734
 QY 121 GGGCTGAAGCGTACGCCCTTCGCTAAGCGGAGCTACGCCCAACCATCTCTGCTGCC 180
 DB 1735 GGGCTGAAGCGTACGCCCTTCGCTAAGCGGAGCTACGCCCAACCATCTCTGCTGCC 1794
 QY 181 CTTTCACATCCATGAGCCCAATGATGCTGTGTACA 216
 DB 1795 CTTTCACATCCATGAGCCCAATGATGCTGTGTACA 1830

RESULT 8
 ID AAS68253 standard; cDNA; 2592 BP.

XX AAS68253;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #4057.

XX Human: chromosome mapping; gene mapping; gene therapy; forensic;

XX food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSPO INC.

XX Drmanac RT, Liu C, Tang YT;

DR WPI: 2001-639362/73.
DR P-PSDB: ABG04066.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
XX
PS Claim 1; SEQ ID No 4057; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 2592 BP; 655 A; 754 C; 659 G; 524 T; 0 other;
Query Match 100.0%; Score 216; DB 23; Length 2592;
Best Local Similarity 100.0%; Pred. No. 3,7e-52;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCGCGCGCGCGCGCGAGAGGGGTGAGTCCATCCAGGCGACAGCTCCAGCCATCTGGC 60
DB 2374 CCGCGCGCGCGCGCGAGAGGGGTGAGTCCATCCAGGCGACAGCTCCAGCCATCTGGC 2433
QY 61 CAGGCGGTGACTGTCTGAGGAGGAGCCAGCTCAAGCGCTAACAATCACTAGACAGGTGG 120
DB 2434 CAGGCGGTGACTGTCTGAGGAGGAGCCAGCTCAAGCGCTAACAATCACTAGACAGGTGG 2493
QY 121 GGGCTGAAGCGTACGCGCTCTAAGCGGAGCTACCCCCCAACATCTCTTGTCTCC 180
DB 2494 GGGCTGAAGCGTACGCGCTCTAAGCGGAGCTACCCCCCAACATCTCTTGTCTCC 2553
QY 181 CTTTCCACATCCATGAAGCCCAATGATGCGGTACA 216
DB 2554 CTTTCCACATCCATGAAGCCCAATGATGCGGTACA 2589
RESULT 9
AAS68807
ID AAS68807 standard; cDNA; 3039 BP.
XX AAS68807;
AC
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #4611.
XX
KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
FN WO200175067-A2.
XX
PD 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR P-PSDB: ABG04620.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
XX
PS Claim 1; SEQ ID No 4611; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 3039 BP; 741 A; 869 C; 781 G; 648 T; 0 other;
Query Match 100.0%; Score 216; DB 23; Length 3039;
Best Local Similarity 100.0%; Pred. No. 3.8e-52;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCGCGCGCGCGCGCGAGAGGGGTGAGTCCATCCAGGCGACAGCTCCAGCCATCTGGC 60
DB 2821 CCGCGCGCGCGCGCGAGAGGGGTGAGTCCATCCAGGCGACAGCTCCAGCCATCTGGC 2880
QY 61 CAGGCGGTGACTGTCTGAGGAGGAGCCAGCTCAAGCGCTAACAATCACTAGACAGGTGG 120
DB 2881 CAGGCGGTGACTGTCTGAGGAGGAGCCAGCTCAAGCGCTAACAATCACTAGACAGGTGG 2940
QY 121 GGGCTGAAGCGTACGCGCTCTAAGCGGAGCTACCCCCCAACATCTCTTGTCTCC 180
DB 2941 GGGCTGAAGCGTACGCGCTCTAAGCGGAGCTACCCCCCAACATCTCTTGTCTCC 3000
QY 181 CTTTCCACATCCATGAAGCCCAATGATGCGGTACA 216
DB 3001 CTTTCCACATCCATGAAGCCCAATGATGCGGTACA 3036
RESULT 10
AAS89721
ID AAS89721 standard; cDNA; 3039 BP.
XX AAS89721;
AC
DT 13-FEB-2002 (first entry)
XX

DE DNA encoding novel human diagnostic protein #25525.
 XX
 KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 XX
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YF;
 XX
 PI WPI; 2001-639362/73.
 DR P-PDB; ABG5534.
 XX
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 1: SEQ ID No 25525; 103bp; English.
 XX
 XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantifying a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging or sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 3039 BP; 741 A; 869 C; 781 G; 648 T; 0 other;
 Query Match 100.0%; Score 216; DB 23; Length 3039;
 Best Local Similarity 100.0%; Pred. No. 3.8e-52;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCGCGCGCGCGCGCGCGAGAGGTGACATCCAGAGTGCACAGCTCCAGCCATCTGCG 60
 DB |||||||
 DB 2821 CCGCGCGCGCGCGCGCGAGAGGTGACATCCAGAGTGCACAGCTCCAGCCATCTGCG 2880
 QY 61 CAGCGCGCGAGTGTCTCGAGGAGCGCCAGCCAGCGTCAACGCTTACACATCTGCAAGGTG 120
 DB |||||||
 DB 2881 CAGCGCGGTACTGTCTCGAGGAGCGCCAGCCAGCTTACACATCTGCAAGGTG 2940
 QY 121 GGGCTGAAGCGTACGCGCTTAAAGCGGAGAGTACCCCAACCATCTTGTGCTCC 180
 DB |||||||
 DB 2941 GGGCTGAAGCGTACGCGCTTAAAGCGGAGAGTACCCCAACCATCTTGTGCTCC 3000
 QY 181 CTTTCACATTCATGAAGCCCAATGATGGGTACA 216
 DB |||||||
 DB 3001 CTTTCACATTCATGAAGCCCAATGATGGGTACA 3036

RESULT 11
 ID AAH17625 standard; cDNA; 3041 BP.
 XX
 AC AAH17625;
 XX
 DT 26-JUN-2001 (first entry)
 XX
 DE Human cDNA sequence SEQ ID NO:17153.
 XX
 KM Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN BP1074617-A2.
 XX
 PD 07-FEB-2001.
 XX
 PF 28-JUL-2000; 2000BP-0116126.
 XX
 PR 29-JUL-1999; 99JP-0248036.
 XX
 PR 27-AUG-1999; 99JP-0300253.
 XX
 PR 11-JAN-2000; 2000JP-0118776.
 XX
 PR 02-MAY-2000; 2000JP-0183767.
 XX
 PR 09-JUN-2000; 2000JP-0241899.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX
 DR WPI; 2001-318749/34.
 XX
 XX Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 XX
 PS Claim 8: SEQ ID 17153; 2537bp + CD ROM; English.
 XX
 XX The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 XX
 SQ Sequence 3041 BP; 804 A; 886 C; 714 G; 637 T; 0 other;
 Query Match 100.0%; Score 216; DB 22; Length 3041;
 Best Local Similarity 100.0%; Pred. No. 3.8e-52;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCGCGCGCGCGCGCGAGAGGTGACATCCAGAGTGCACAGCTCCAGCCATCTGCG 60
 DB |||||||

Db 1966 CCGCGCCGCCGCCGAGAGGGTGGACTCCATCCAGGTGACACAGTCCACAGCCATCTGGC 2025
 QY 61 CAGCGCGTGAAGTCTGCTGAGGAGAGCCAGCCCTCAAGCCCTACAGACACACAGAGGTGC 120
 Db 2026 CAGCGCGTGAAGTCTGCTGAGGAGAGCCAGCCCTCAAGCCCTACAGACACACAGAGGTGC 2085
 QY 121 GGGCTGAAGCGTGAAGCGCCCTGCTAAAGCCGAGAGTACCCCAACCATCTTGGTCCC 180
 Db 2086 GGGCTGAAGCGTGAAGCGCCCTGCTAAAGCCGAGAGTACCCCAACCATCTTGGTCCC 2145
 QY 181 CTTTCCATCATCATGAAGCCCAATGATGCGGTACA 216
 Db 2146 CTTTCCATCATCATGAAGCCCAATGATGCGGTACA 2181

RESULT 12
 AAA93618
 ID AAA93618 standard; DNA: 3333 BP.
 AC AAA93618;
 XX
 DT 16-JAN-2001 (first entry)
 DE Human semaphorin protein-like splice variant SECX 2864933-2 DNA.
 XX
 KW SECX protein; human; secreted; membrane-associated; cancer;
 KW proliferation regulator; differentiation regulator; non-malignant tumour;
 KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;
 KW infection; inflammatory disorder; arthritis; haematopoietic disorder;
 KW skin disorder; cardiovascular disorder; atherosclerosis; restenosis;
 KW neurological disease; Alzheimer's disease; trauma; wounding;
 KW spinal cord injury; skeletal disorder; cystostatic; immunosuppressive;
 KW anti-HIV; antiinflammatory; antiatheritic; antiarteriosclerotic;
 KW neuroprotective; vulnery; antiallergic; antimicrobial; cardiant;
 KW dermatological; gene therapy; ds.
 XX
 OS Homo sapiens.
 PN WO200053742-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 09-MAR-2000; 2000MO-US06280.
 XX
 PR 09-MAR-1999; 9905-0123667.
 XX
 PR 08-MAR-2000; 2000US-0123667.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA;
 XX
 DR WPI: 2000-594318/56.
 XX
 DR P-PSDB: AAB23031.
 XX
 PT Novel human membrane associated or secreted polypeptides and
 PT polynucleotides useful for diagnosis, prevention and treatment of
 PT pathological states such as cancer, immune, cardiovascular and
 PT neurological disorders
 XX
 PS Claim 3; Fig 3; 151pp; English.
 XX
 CC Sequences AAA93618-A93631 and AAA93673-A93676 represent nucleic acids
 CC which encode human SECX proteins (AAB23029-B23048). The SECX proteins
 CC of the invention are either secreted or membrane-associated proteins
 CC and act as regulator of cellular proliferation and differentiation. SECX
 CC proteins or nucleotides are useful for diagnosing the presence of, or
 CC predisposition to, a disease associated with altered levels of SECX
 CC proteins and nucleotides. The SECX proteins are also useful to screen
 CC compounds that modulate SECX activity or expression. The interaction of
 CC a SECX protein with other cellular proteins may be useful to modulate
 CC the activity of a partner protein, cellular proliferation, cellular
 CC differentiation and cell survival. SECX nucleotides are useful for the
 CC recombinant expression of SECX protein, and may be used detect SECX mRNA

CC or genetic lesions in the SECX gene. They may also be used to modulate
 CC SECX expression (e.g., using antisense oligonucleotides). SECX nucleic
 CC acid sequences are also useful for identifying a cell or tissue type in
 CC a biological sample, and in forensic biology. SECX primers or probes are
 CC useful for detecting the presence of SECX nucleotides and for screening
 CC tissue cultures for contamination. Diseases that may be treated or
 CC prevented using SECX proteins or nucleotides include cancer (e.g.,
 CC colorectal carcinoma, prostate cancer), benign tumours, immune disorders
 CC (including autoimmune diseases, transplant rejection, allergies, AIDS),
 CC infections, inflammatory disorders, arthritis, haematopoietic disorders,
 CC skin disorders, cardiovascular disorders, atherosclerosis, restenosis,
 CC neurological diseases (e.g., Alzheimer's disease), trauma (e.g.,
 CC surgical or traumatic wounds, spinal cord injury), and skeletal
 CC disorders.
 XX
 SQ Sequence 3333 BP; 874 A; 921 C; 845 G; 692 T; 1 other;
 Query Match 100.0%; Score 216; DB 21; Length 3333;
 Best Local Similarity 100.0%; Pred. No. 3,9e-52;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCGCCGCCGCCGAGAGGGTGGACTCCATCCAGGTGACACAGTCCACAGCCATCTGGC 60
 Db 2925 CCGCGCCGCCGCCGAGAGGGTGGACTCCATCCAGGTGACACAGTCCACAGCCATCTGGC 2984
 QY 61 CAGCGCGTGAAGTCTGCTGAGGAGAGCCAGCCCTCAAGCCCTACAGACACACAGAGGTGC 120
 Db 2985 CAGCGCGTGAAGTCTGCTGAGGAGAGCCAGCCCTCAAGCCCTACAGACACACAGAGGTGC 3044
 QY 121 GGGCTGAAGCGTGAAGCGCCCTGCTAAAGCCGAGAGTACCCCAACCATCTTGGTCCC 180
 Db 3045 GGGCTGAAGCGTGAAGCGCCCTGCTAAAGCCGAGAGTACCCCAACCATCTTGGTCCC 3104
 QY 181 CTTTCCATCATCATGAAGCCCAATGATGCGGTACA 216
 Db 3105 CTTTCCATCATCATGAAGCCCAATGATGCGGTACA 3140

RESULT 13
 AAA93617
 ID AAA93617 standard; DNA: 3498 BP.
 AC AAA93617;
 XX
 DT 16-JAN-2001 (first entry)
 DE Human semaphorin protein-like splice variant SECX 2864933-1 DNA.
 XX
 KW SECX protein; human; secreted; membrane-associated; cancer;
 KW proliferation regulator; differentiation regulator; non-malignant tumour;
 KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;
 KW infection; inflammatory disorder; arthritis; haematopoietic disorder;
 KW skin disorder; cardiovascular disorder; atherosclerosis; restenosis;
 KW neurological disease; Alzheimer's disease; trauma; wounding;
 KW spinal cord injury; skeletal disorder; cystostatic; immunosuppressive;
 KW anti-HIV; antiinflammatory; antiatheritic; antiarteriosclerotic;
 KW neuroprotective; vulnery; antiallergic; antimicrobial; cardiant;
 KW dermatological; gene therapy; ds.
 XX
 OS Homo sapiens.
 PN WO200053742-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 09-MAR-2000; 2000MO-US06280.
 XX
 PR 09-MAR-1999; 9905-0123667.
 XX
 PR 08-MAR-2000; 2000US-0123667.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA;

Search completed: September 30, 2003, 16:58:39
 UOD time : 59.8323 secs

```

AC  AAF98469;
XX
DT  07-JUN-2001 (first entry)
XX
DE  Human cDNA clone CJ145_1 sequence SEQ ID 160.
XX
KW  Human; secreted protein; nutrient; cytokine modulator; proliferation;
KW  differentiation; immune system modulator; tissue growth; chemotactic;
KW  haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ss;
KW  haematopoiesis.
XX
OS  Homo sapiens.
XX
PN  W0200119988-A1.
XX
PD  22-MAR-2001.
XX
PF  14-SEP-2000; 2000WO-US25135.
XX
PR  17-SEP-1999; 99US-0398829.
XX
PA  (GEMV ) GENETICS INST INC.
XX
PI  Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;
PI  Merberg D, Treacy M, Bowman MR, Spaulding V, Agostino MJ;
XX
DR  MPI: 2001-244801/25.
DR  P-PSDB: AAB90731.
XX
PT  Isolated nucleic acids encoding polypeptides, useful for modulating
PT  e.g. cytokine and cell proliferation/differentiation activity, the
PT  immune system and hematopoiesis regulating activity -
XX
PS  Disclosure; Page 486-487; 557pp; English.
XX
CC  Human cDNA clones represented in AAF98374 - AAF98489 encode secreted
CC  proteins AAB90667 - AAB90750. The cDNA clones are isolated from various
CC  tissue types, and may be used in the prevention, treatment and diagnosis
CC  of diseases associated with inappropriate protein expression. The
CC  polypeptides and nucleic acids may be used as nutrients or to modulate
CC  cytokine and cell proliferation/differentiation activity and may also be
CC  involved in modulation of the immune system. The cDNA sequences,
CC  proteins, their agonists and/or antagonists exhibit haematopoiesis
CC  regulating activity; tissue growth activity; activin/inhibin activity;
CC  chemotactic/chemokinetic activity; haemostatic and thrombolytic
CC  activity; receptor/ligand activity; anti-inflammatory activity;
CC  haematopoiesis activity; cadherin/tumour suppressor activity; and/or
CC  tumour inhibition activity. Included in the invention are probes
CC  represented in AAF98490 - AAF98572 which are specific for the cDNA clones
CC  encoding the secreted proteins.
XX
SQ  Sequence 3550 BP; 957 A; 994 C; 856 G; 742 T; 1 other;

Query Match      100.0%; Score 216; DB 22; Length 3550;
Best Local Similarity 100.0%; Pred. No. 4e-52;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1  CCGCGCGCGCGCGCGAGAGGCTGACATCCAGGTGCACAGCTCCAGCCACTGGC 60
    |||||||
DB  2835  CCGCGCGCGCGCGCGAGAGGCTGACATCCAGGTGCACAGCTCCAGCCACTGGC 2894
    |||||||

QY  61  CAGGCCGTGACTGTCTCGAGGAGCCGCTCAACGGCTCAACTCACTGACAAGTGC 120
    |||||||
DB  2895  CAGGCCGTGACTGTCTCGAGGAGCCGCTCAACGGCTCAACTCACTGACAAGTGC 2954
    |||||||

QY  121  GGGCTGAAGCGTAGCCCTCGCTAAAGCCGGAGGTACCCCAAAACATCTTGTCTCC 180
    |||||||
DB  2955  GGGCTGAAGCGTAGCCCTCGCTAAAGCCGGAGGTACCCCAAAACATCTTGTCTCC 3014
    |||||||

QY  181  CTTTCACATCCATGAGGCCCAATGATGGGTGATCA 216
    |||||||
DB  3015  CTTTCACATCCATGAGGCCCAATGATGGGTGATCA 3050
    |||||||
  
```


SEQUENCE CHARACTERISTICS:
 LENGTH: 43280 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 816..14234
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 14351..19945
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 20010..31199
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 31232..36067
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 36249..41774
 US-08-804-227C-1

Query Match 16.3%; Score 35.2; DB 2; Length 43280;
 Best Local Similarity 48.5%; Pred. No. 0.78;
 Matches 97; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 2 CGCCGCCGCCCGCCGAGAGGGTGGACTCCATCCAGTGCACAGCTCCCAAGCCATGTGGCC 61
 DB 1896 CGCCGAGGGGGCTGTGGGGCGCTGCCGCCGCCGCCGCCGCCGCCGCCGAGTGGGG 1837
 QY 62 AGGCGGTACTGTCTCGAGAGCGCCAGCCCTCAACGCTACAACTGACAGAGTGGG 121
 DB 1836 CGCCTTCGACGGGGGTGCGCGGCGCGGTGCGGTCCCTGCACTGACGTAGCGGAGCG 1777
 QY 122 GGCTGAAGCGTACGCCCTGCTTAAAGCGGACGTACCCCAAAACCATCTTTGCTCCCG 181
 DB 1776 CGCCGGTGTGACGCCCGCCCGCGGTAGGCTGCGGAGCAGACACTTCTGCGCTCCG 1717
 QY 182 TTTCACATCCATGAGGCC 201
 DB 1716 GGTGCGGAGTGTGAGGCTC 1697

RESULT 5

US-09-103-840A-2/c
 ; Sequence 2, Application US/09103840A
 ; Patent No. 6294328
 ; GENERAL INFORMATION:
 ; APPLICANT: FLEISCHMAN, Robert D.
 ; APPLICANT: WHITE, Owen R.
 ; APPLICANT: FRASER, Claire M.
 ; APPLICANT: VENTER, John C.
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 ; FILE REFERENCE: 24366-2007.00
 ; CURRENT APPLICATION NUMBER: US/09/103,840A
 ; CURRENT FILING DATE: 1998-06-24
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 4403765
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium tuberculosis
 ; FEATURE:
 ; OTHER INFORMATION: CDC 1551
 ; OTHER INFORMATION: "n" bases at various positions throughout the sequence
 ; OTHER INFORMATION: represent a, t, c or g
 US-09-103-840A-2

Query Match 15.9%; Score 34.4; DB 3; Length 4403765;
 Best Local Similarity 57.4%; Pred. No. 4.2;
 Matches 62; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 22 GTGACTCATCCAGGTGACAGCTCCAGCCATCGTGGCCAGCCGTGACTGTCTGAGG 81
 DB 745995 GGGTATTCCTCTGTAAGAGGCCAGCTGCTGGCTACCCGCCGCGCGATCAGCTGGCGG 745936
 QY 82 CAGCCAGCCTCAAGCCCTACAACTCACTGACAGAGTGGGGCTGAAG 129
 DB 745935 CCGTCTGTGACAGGAGGACAAAGCCCGCCAGCCTGSGGGTGCAGC 745888

RESULT 6

US-09-103-840A-1/c
 ; Sequence 1, Application US/09103840A
 ; Patent No. 6294328
 ; GENERAL INFORMATION:
 ; APPLICANT: FLEISCHMAN, Robert D.
 ; APPLICANT: WHITE, Owen R.
 ; APPLICANT: FRASER, Claire M.
 ; APPLICANT: VENTER, John C.
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 ; FILE REFERENCE: 24366-2007.00
 ; CURRENT APPLICATION NUMBER: US/09/103,840A
 ; CURRENT FILING DATE: 1998-06-24
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 4411529
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium tuberculosis
 ; OTHER INFORMATION: H37Rv
 US-09-103-840A-1

Query Match 15.9%; Score 34.4; DB 3; Length 4411529;
 Best Local Similarity 57.4%; Pred. No. 4.2;
 Matches 62; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 22 GTGACTCATCCAGGTGACAGCTCCAGCCATCGTGGCCAGCCGTGACTGTCTGAGG 81
 DB 744035 GGGTATTCCTCTGTAAGAGGCCAGCTGCTGGCTACCCGCCGCGCGATCAGCTGGCGG 743976
 QY 82 CAGCCAGCCTCAAGCCCTACAACTCACTGACAGAGTGGGGCTGAAG 129
 DB 743975 CCGTCTGTGACAGGAGGACAAAGCCCGCCAGCCTGSGGGTGCAGC 743928

RESULT 7

US-09-252-991A-8905/c
 ; Sequence 8905, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 8905
 ; LENGTH: 846
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-8905

Query Match 15.6%; Score 33.8; DB 4; Length 846;
 Best Local Similarity 49.2%; Pred. No. 0.72;
 Matches 89; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

```
Db 343 CTTGGAGCGCCGACACATCTTCTGGCCATCGCTTGGCGCGCGGCGAGGTGGCGGGG 284
QY 62 AGGCGGTGATGTCTGTGAGGACAGCCCAAGCTCAAGCCTACAACTACTGACAGGTGG 121
Db 283 CTTCCGGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 224
QY 122 GGTGAAGCGTACGCGCTGCTTAAGCCGAGCTACCCCGCAACATCTTGTCTCCG 181
Db 223 CCAGCCAGCGTTTACGCTACGTATCTGCTGCGAGGCGCCCGCGAGCCAGCGCTGATGTGG 164
QY 182 T 182
Db 163 T 163
```

```
RESULT 8
US-09-252-991A-1737
; Sequence 1737, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/094,788
; PRIOR FILING DATE: 1998-07-27
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1737
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1737
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Query Match 15.6%; Score 33.8; DB 4; Length 1026;
Best Local Similarity 54.4%; Pred. No. 0.76;
Matches 68; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
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QY 62 AGGCGGTGATGTCTGTGAGGACAGCCCAAGCTCAAGCCTACAACTACTGACAGGTGG 121
Db 271 AGGCGGTGATGTCTGTGAGGACAGCCCAAGCTCAAGCCTACAACTACTGACAGGTGG 330
QY 122 GGTGAAGCGTACGCGCTGCTTAAGCCGAGCTACCCCGCAACATCTTGTCTCCG 181
Db 331 GGTGAAGCGTACGCGCTGCTTAAGCCGAGCTACCCCGCAACATCTTGTCTCCG 390
QY 182 TTTC 186
Db 391 TTTC 395
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```
RESULT 9
US-09-252-991A-9254
; Sequence 9254, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/094,788
; PRIOR FILING DATE: 1998-07-27
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9254
; LENGTH: 2667
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; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9254
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Query Match 15.6%; Score 33.8; DB 4; Length 2667;
Best Local Similarity 49.2%; Pred. No. 0.96;
Matches 89; Conservative 0; Mismatches 92; Indels 0; Gaps 0;
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QY 2 CGCGCGCGCGCGCGGAGAGGAGTGCATCCATGACAGTGCACAGTCCGACGATCTGGCC 61
Db 38 CTTGGAGCGCCGACACATCTTCTGGCCATCGCTTGGCGCGCGGCGAGGTGGCGGGG 97
QY 62 AGGCGGTGATGTCTGTGAGGACAGCCCAAGCTCAAGCCTACAACTACTGACAGGTGG 121
Db 98 CTTCCGGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 157
QY 122 GGTGAAGCGTACGCGCTGCTTAAGCCGAGCTACCCCGCAACATCTTGTCTCCG 181
Db 158 CCAGCCAGCGTTTACGCTACGTATCTGCTGCGAGGCGCCCGCGAGCCAGCGCTGATGTGG 217
QY 182 T 182
Db 218 T 218
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```
RESULT 10
US-09-252-991A-1816
; Sequence 1816, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/094,788
; PRIOR FILING DATE: 1998-07-27
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1816
; LENGTH: 3228
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1816
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Query Match 15.6%; Score 33.8; DB 4; Length 3228;
Best Local Similarity 54.4%; Pred. No. 1;
Matches 68; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
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QY 62 AGGCGGTGATGTCTGTGAGGACAGCCCAAGCTCAAGCCTACAACTACTGACAGGTGG 121
Db 303 AGGCGGTGATGTCTGTGAGGACAGCCCAAGCTCAAGCCTACAACTACTGACAGGTGG 362
QY 122 GGTGAAGCGTACGCGCTGCTTAAGCCGAGCTACCCCGCAACATCTTGTCTCCG 181
Db 363 GGTGAAGCGTACGCGCTGCTTAAGCCGAGCTACCCCGCAACATCTTGTCTCCG 422
QY 182 TTTC 186
Db 423 TTTC 427
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RESULT 11
US-09-252-991A-2143/C
; Sequence 2143, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
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;; CURRENT APPLICATION NUMBER: US/09/252,991A
;; PRIOR FILING DATE: 1999-02-18
;; PRIOR APPLICATION NUMBER: US 60/074,788
;; PRIOR FILING DATE: 1998-02-18
;; PRIOR APPLICATION NUMBER: US 60/094,190
;; PRIOR FILING DATE: 1998-07-27
;; NUMBER OF SEQ ID NOS: 33142
;; SEQ ID NO 2143
;; LENGTH: 3546
;; TYPE: DNA
;; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2143

Query Match 15.6%; Score 33.8; DB 4; Length 3546;
Best Local Similarity 54.4%; Pred. No. 1;
Matches 68; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 62 AGCCGTCGACCTGCTCGAGGCGAGCCGCTCAAGCCCTACAGCTCACTGACAGAGGTGG 121
DB 3064 AGCCGCGATCAACATCAAGAGAGTCTTGAAGCCAGGAGGAGTATCTGCTGAGTCA 3005
QY 122 GGCTGAAGCGTACGCGCTCGCTGAAGCGGAGTACCCCGCAACCATCTTGTCTCCG 181
DB 3004 GAAGAGAGAGCGCGGCAACAGGCGCGCCCTGACCACTTCATCAGCTGGCGCGCG 2945
QY 182 TTTC 186
DB 2944 TTAC 2940

RESULT 12

US-09-252-991A-7012/c
;; Sequence 7012, Application US/09252991A
;; Patent No. 6551795
;; GENERAL INFORMATION:
;; APPLICANT: Marc J. Rubenfield et al.
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;; FILE REFERENCE: 107196.136
;; CURRENT APPLICATION NUMBER: US/09/252,991A
;; PRIOR FILING DATE: 1999-02-18
;; PRIOR APPLICATION NUMBER: US 60/074,788
;; PRIOR FILING DATE: 1998-02-18
;; PRIOR APPLICATION NUMBER: US 60/094,190
;; PRIOR FILING DATE: 1998-07-27
;; NUMBER OF SEQ ID NOS: 33142
;; SEQ ID NO 7012
;; LENGTH: 630
;; TYPE: DNA
;; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7012

Query Match 15.4%; Score 33.2; DB 4; Length 630;
Best Local Similarity 53.0%; Pred. No. 0.99;
Matches 71; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 7 CCGGCCCCGAGAGGTGAGTCCATCCAGTGCAGCTCCAGCCATCTGGCCAGGCC 66
DB 203 CCGGCGGCGATCGAGTGTGATGCGGCGATCGCCCGCTCCGCGCTGGCTGGCG 144
QY 67 GTGACTGTCTCGAGGAGCCAGGCTCAAGGCTCAACTCACTGACAGAGTGGGGCTG 126
DB 143 CATCTATCTGTGAGGCGCGCCCATGAGCATGAGCTTCAGGCCCTTCCCAAGAGGCGCGAC 84
QY 127 AAGCTAGCCCTC 140
DB 83 AGGCACTGCGCCCTC 70

RESULT 13
US-09-252-991A-7061
;; Sequence 7061, Application US/09252991A
;; Patent No. 6551795

;; GENERAL INFORMATION:
;; APPLICANT: Marc J. Rubenfield et al.
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA
;; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;; FILE REFERENCE: 107196.136
;; CURRENT APPLICATION NUMBER: US/09/252,991A
;; PRIOR FILING DATE: 1999-02-18
;; PRIOR APPLICATION NUMBER: US 60/074,788
;; PRIOR FILING DATE: 1998-02-18
;; PRIOR APPLICATION NUMBER: US 60/094,190
;; PRIOR FILING DATE: 1998-07-27
;; NUMBER OF SEQ ID NOS: 33142
;; SEQ ID NO 7061
;; LENGTH: 1548
;; TYPE: DNA
;; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7061

Query Match 15.4%; Score 33.2; DB 4; Length 1548;
Best Local Similarity 53.0%; Pred. No. 1.2;
Matches 71; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 7 CCGGCCCCGAGAGGTGAGTCCATCCAGTGCAGAGCTCCAGCCATCTGGCCAGGCC 66
DB 532 CCGGCGGCGATCGAGTGTGATGCGGCGATCGCCCGCTCCGCGCGCTGGCTGGCG 591
QY 67 GTGACTGTCTCGAGGAGCCAGGCTCAAGGCTCAACTCACTGACAGAGTGGGGCTG 126
DB 592 CATCTATCTGTGAGGCGCGCCCATGAGCATGAGCTTCAGGCCCTTCCCAAGAGGCGCGAC 651
QY 127 AAGCTAGCCCTC 140
DB 652 AGGCACTGCGCCCTC 665

RESULT 14

US-09-252-991A-7117
;; Sequence 7117, Application US/09252991A
;; Patent No. 6551795
;; GENERAL INFORMATION:
;; APPLICANT: Marc J. Rubenfield et al.
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA
;; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;; FILE REFERENCE: 107196.136
;; CURRENT APPLICATION NUMBER: US/09/252,991A
;; PRIOR FILING DATE: 1999-02-18
;; PRIOR APPLICATION NUMBER: US 60/074,788
;; PRIOR FILING DATE: 1998-02-18
;; PRIOR APPLICATION NUMBER: US 60/094,190
;; PRIOR FILING DATE: 1998-07-27
;; NUMBER OF SEQ ID NOS: 33142
;; SEQ ID NO 7117
;; LENGTH: 1581
;; TYPE: DNA
;; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7117

Query Match 15.4%; Score 33.2; DB 4; Length 1581;
Best Local Similarity 53.0%; Pred. No. 1.3;
Matches 71; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 7 CCGGCCCCGAGAGGTGAGTCCATCCAGTGCAGAGCTCCAGCCATCTGGCCAGGCC 66
DB 623 CCGGCGGCGATCGAGTGTGATGCGGCGATCGCCCGCTCCGCGCGCTGGCTGGCG 682
QY 67 GTGACTGTCTCGAGGAGCCAGGCTCAAGGCTCAACTCACTGACAGAGTGGGGCTG 126
DB 683 CATCTATCTGTGAGGCGCGCCCATGAGCATGAGCTTCAGGCCCTTCCCAAGAGGCGCGAC 742
QY 127 AAGCTAGCCCTC 140
DB 743 AGGCACTGCGCCCTC 756


```
RESULT 15
US-08-993-359-29
; Sequence 29, Application US/08993359A
; Patent No. 603942
; GENERAL INFORMATION:
; APPLICANT: Lassen, Soren F.
; APPLICANT: Bech, Lisbeth
; APPLICANT: Ohmann, Anders
; APPLICANT: Breinholt, Jens
; APPLICANT: Fuglsang, Claus C.
; APPLICANT: Ostergaard, Peter R.
; TITLE OF INVENTION: Phylase Polypeptides
; FILE REFERENCE: 5383 500-US
; CURRENT APPLICATION NUMBER: US/08/993,359A
; CURRENT FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 1480/96
; EARLIER FILING DATE: 1996-12-20
; EARLIER APPLICATION NUMBER: 1481/96
; EARLIER FILING DATE: 1996-12-20
; EARLIER APPLICATION NUMBER: 0301/97
; EARLIER FILING DATE: 1997-03-18
; EARLIER APPLICATION NUMBER: 0529/97
; EARLIER FILING DATE: 1997-05-07
; EARLIER APPLICATION NUMBER: 1388/97
; EARLIER FILING DATE: 1997-12-01
; EARLIER APPLICATION NUMBER: 60/046,082
; EARLIER FILING DATE: 1997-05-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 1536
; TYPE: DNA
; ORGANISM: Trametes pubescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (79)...(1407)
; NAME/KEY: mat.peptide
; LOCATION: (130)...(1407)
; NAME/KEY: sig.peptide
; LOCATION: (79)...(129)
US-08-993-359-29

Query Match      15.3%; Score 33; DB 3; Length 1536;
Best Local Similarity 53.5%; Pred. No. 14;
Matches 69; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY      11  CCCCAGAGAGGCTGAGCTCATCCAGTGACAGAGCTCCAGCCATCTGCGCGGTGA 70
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      950  CCGTGCAAGGCGTCCGGTACATCAAGAGCTCATCGCGGCTCACCGCGAGACGTGT 1009
QY      71  CTGTCGAGGAGCCCGCAAGCCTCAAGCGCTACACTCACTGACAAAGTGGGGCTGAAGC 130
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      1010 CCGACACACGAGAGAGACAGACACACTGACTCTCGCCGAGAGAGTTCCCGCTCAACC 1069
QY      131  GTAGGCCCT 139
      ||||| |||
DB      1070 GCACGCTCT 1078
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Search completed: September 30, 2003, 22:06:17
Job time : 27.4914 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	216	100.0	1472	9	US-09-925-299-60	Sequence 60, Appl1
2	216	100.0	1472	11	US-09-925-299-60	Sequence 60, Appl1
3	216	100.0	3333	11	US-09-991-053-5	Sequence 5, Appl1
4	216	100.0	3333	11	US-09-957-187-5	Sequence 5, Appl1
5	216	100.0	3498	11	US-09-991-053-3	Sequence 3, Appl1
6	216	100.0	3498	11	US-09-957-187-3	Sequence 3, Appl1
7	216	100.0	4250	11	US-09-957-187-84	Sequence 84, Appl1
8	168	77.8	460	11	US-09-918-985-3799	Sequence 3799, Appl1
9	55	25.5	6767	11	US-09-764-891-6944	Sequence 6944, Appl1
10	55	25.5	6773	11	US-09-764-891-6943	Sequence 6943, Appl1
11	53.4	24.7	662	11	US-09-764-891-810	Sequence 810, Appl1
12	37.4	17.3	765	13	US-10-027-632-166826	Sequence 166826, Appl1
13	35.4	16.4	1971	10	US-09-554-000-7	Sequence 7, Appl1
14	35.2	16.3	936	14	US-10-128-714-1578	Sequence 7578, Appl1
15	35.2	16.3	936	14	US-10-128-714-1578	Sequence 7578, Appl1
16	35.2	16.3	1015	14	US-10-128-714-1578	Sequence 1578, Appl1

17	35.2	16.3	1015	14	US-10-128-714-6578	Sequence 6578, App
18	35.2	16.3	3015	14	US-10-128-714-5578	Sequence 5578, App
19	35.2	16.3	3015	14	US-10-128-714-5578	Sequence 5578, App
20	33.6	15.6	3970	14	US-10-158-646-9	Sequence 9, Appl1
21	33.2	15.4	936	14	US-10-187-267A-34	Sequence 34, Appl1
22	33.2	15.4	1458	14	US-10-156-761-6684	Sequence 6684, App
23	33.2	15.4	36321	14	US-10-187-267A-1	Sequence 1, Appl1
24	33.2	15.4	9025608	14	US-10-156-761-1	Sequence 1, Appl1
25	32.8	15.2	1133	14	US-10-156-761-1908	Sequence 1908, App
26	32.8	15.2	9025608	14	US-10-156-761-1	Sequence 1, Appl1
27	32.4	15.0	1167	14	US-10-156-761-1	Sequence 541, App
28	32	14.8	519	9	US-09-864-761-22733	Sequence 22733, App
29	32	14.8	1095	12	US-09-109-203A-4	Sequence 4, Appl1
30	32	14.8	1162	14	US-10-037-270-982	Sequence 982, App
31	32	14.8	1172	12	US-10-139-672-209	Sequence 209, App
32	32	14.8	1172	12	US-10-187-749-209	Sequence 209, App
33	32	14.8	1172	12	US-10-194-457-209	Sequence 209, App
34	32	14.8	1172	12	US-10-184-644-209	Sequence 209, App
35	32	14.8	1172	12	US-10-196-747-209	Sequence 209, App
36	32	14.8	1172	12	US-10-173-689-209	Sequence 209, App
37	32	14.8	1172	12	US-10-173-696-209	Sequence 209, App
38	32	14.8	1172	12	US-10-173-691-209	Sequence 209, App
39	32	14.8	1172	12	US-10-173-692-209	Sequence 209, App
40	32	14.8	1172	12	US-10-173-694-209	Sequence 209, App
41	32	14.8	1172	12	US-10-173-698-209	Sequence 209, App
42	32	14.8	1172	12	US-10-173-699-209	Sequence 209, App
43	32	14.8	1172	12	US-10-173-707-209	Sequence 209, App
44	32	14.8	1172	12	US-10-174-556-209	Sequence 209, App
45	32	14.8	1172	12	US-10-174-583-209	Sequence 209, App

ALIGNMENTS

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1
US-09-925-299-60
; Sequence 60, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Prote
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,29
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 1472
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (129)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (130)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-60

```

Query Match	100.0%	Score 216;	DB 9;	length 1472;
Best Local Similarity	100.0%	Pred. No. 5.1e-58;		
Matches 216;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	CCGCGCGCCGCCG	CAGAGGGTGGACT	CCATCCAGGTGC	ACAGCTCCAGCC	ACTCTGGC	60
DB	372	CCGCGCGCCGCCG	CAGAGGGTGGACT	CCATCCAGGTGC	ACAGCTCCAGCC	ACTCTGGC	431
QY	61	CAGGCGGTGACTG	TCTGAGGACGCC	CCCATCAAGCGCT	CAACGCTCAACTC	ACTATCAGAGTCG	120

Db 432 CAGGCCGTGACTGTCTGAGAGGAGCCAGCCCTCAAGGCTTACAACTCACTGACAGGTG 491
QY 121 GGGCTGAAGCGTAGCCCTCGCTAAAGCGGAGCGATACCCCAACCAATCTTGTCTGCC 180
Db 492 GGGCTGAAGCGTAGCCCTCGCTAAAGCGGAGCGATACCCCAACCAATCTTGTCTGCC 551
QY 181 CTTTCCACATCCATGAAGCCCAATGATGCTGTACA 216
Db 552 CTTTCCACATCCATGAAGCCCAATGATGCTGTACA 587

RESULT 2
US-09-925-299-60
; Sequence 60, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 1472
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (129)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc.feature
; LOCATION: (130)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-60

Query Match 100.0%; Score 216; DB 11; Length 1472;
Best Local Similarity 100.0%; Pred. No. 5.1e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCGCCGCGCCCGCAGAGGAGGTGACTTCATCCAGGTGACAGTCCAGCCATCTGAC 60
Db 372 CCGCGCCGCGCCCGCAGAGGAGGTGACTTCATCCAGGTGACAGTCCAGCCATCTGAC 431
QY 61 CAGGCCGTGACTGTCTGAGAGGAGCCAGCCCTCAAGGCTTACAACTCACTGACAGGTG 120
Db 432 CAGGCCGTGACTGTCTGAGAGGAGCCAGCCCTCAAGGCTTACAACTCACTGACAGGTG 491
QY 121 GGGCTGAAGCGTAGCCCTCGCTAAAGCGGAGCGATACCCCAACCAATCTTGTCTGCC 180
Db 492 GGGCTGAAGCGTAGCCCTCGCTAAAGCGGAGCGATACCCCAACCAATCTTGTCTGCC 551
QY 181 CTTTCCACATCCATGAAGCCCAATGATGCTGTACA 216
Db 552 CTTTCCACATCCATGAAGCCCAATGATGCTGTACA 587

RESULT 3
US-09-991-053-5
; Sequence 5, Application US/09991053
; Publication No. US20030003532A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES ENCODING HUMAN SLIT-,
; FILE REFERENCE: 15966-540 CON S-10
; CURRENT APPLICATION NUMBER: US/09/991,053
; CURRENT FILING DATE: 2002-05-23
; OTHER INFORMATION: an n may be any one of a or t or g or c
; PRIOR APPLICATION NUMBER: USSN 60/123,667

; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 3333
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)..(2865)
; NAME/KEY: misc.feature
; LOCATION: (2882)
; OTHER INFORMATION: an n may be any one of a or t or g or c
US-09-991-053-5

Query Match 100.0%; Score 216; DB 11; Length 3333;
Best Local Similarity 100.0%; Pred. No. 5.5e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCGCCGCGCCCGCAGAGGAGGTGACTTCATCCAGGTGACAGTCCAGCCATCTGAC 60
Db 2925 CCGCGCCGCGCCCGCAGAGGAGGTGACTTCATCCAGGTGACAGTCCAGCCATCTGAC 2984
QY 61 CAGGCCGTGACTGTCTGAGAGGAGCCAGCCCTCAAGGCTTACAACTCACTGACAGGTG 120
Db 2985 CAGGCCGTGACTGTCTGAGAGGAGCCAGCCCTCAAGGCTTACAACTCACTGACAGGTG 3044
QY 121 GGGCTGAAGCGTAGCCCTCGCTAAAGCGGAGCGATACCCCAACCAATCTTGTCTGCC 180
Db 3045 GGGCTGAAGCGTAGCCCTCGCTAAAGCGGAGCGATACCCCAACCAATCTTGTCTGCC 3104
QY 181 CTTTCCACATCCATGAAGCCCAATGATGCTGTACA 216
Db 3105 CTTTCCACATCCATGAAGCCCAATGATGCTGTACA 3140

RESULT 4

US-09-957-187-5
; Sequence 5, Application US/09957187
; Publication No. US20030054514A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
; FILE REFERENCE: 15966-540 CIP
; CURRENT APPLICATION NUMBER: US/09/957,187
; CURRENT FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 3333
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)..(2865)
; NAME/KEY: misc.feature
; LOCATION: (2882)
; OTHER INFORMATION: an n may be any one of a or t or g or c
US-09-957-187-5

Query Match:	100.0%;	Score 216;	DB 11;	Length 3333;
Best Local Similarity:	100.0%;	Pred. No. 5.5e-58;		
Matches 216;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	CCGCGCCGCCCCCGCAGAGAGGTGGAGTCCATCCAGGTGCGACAGCTCCAGCAGTCAGTGGC	60
Db	2925	CCGCGCCGCCCCCGCAGAGAGGTGGAGTCCATCCAGGTGCGACAGCTCCAGCAGTCAGTGGC	2988
QY	61	CAGGCGGTGACTGTCTCTGAGGAGCAGCCAGCCTCTCAAGCGCTCAACTCACTGACAGAAGTGG	120
Db	2985	CAGGCGGTGACTGTCTCTGAGGAGCAGCCAGCCTCTCAAGCGCTCAACTCACTGACAGAAGTGG	3044
QY	121	GGGCTGAAGGCTACGGCCCTCGCTAAAGCCGAGGTACCCGCCAAACATCTTTGCTGCC	180
Db	3045	GGGCTGAAGGCTACGGCCCTCGCTAAAGCCGAGGTACCCGCCAAACATCTTTGCTGCC	3104
QY	181	CTTTCACATTCATGAAGCCCAATGATGCGGTGACA	216
Db	3105	CTTTCACATTCATGAAGCCCAATGATGCGGTGACA	3140

RESULT 5
US-09-991-053-3

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Publication No. US20030003532A1
GENERAL INFORMATION:
APPLICANT: Shinketsu, Richard A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES ENCODING HUMAN SLIT-,
FILE REFERENCE: 15966-540 CON 5-10
CURRENT APPLICATION NUMBER: US/09/991,053
PRIORITY FILING DATE: 2002-05-23
PRIORITY FILING DATE: 1999-03-09
PRIORITY APPLICATION NUMBER: 09/520,781
PRIORITY FILING DATE: 2000-03-08
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 3498
Type: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (214)..(3030)
FEATURE:
NAME/KEY: misc-feature
LOCATION: (3047)
OTHER INFORMATION: an n may be any one of a or t or g or c
US-09-991-053-3

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Query Match	100.0%;	Score 216;	DB 11;	Length 3498;
Best Local Similarity	100.0%;	Pred. No. 5.5e-58;		
Matches 216;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY	Db	QY	Db
1	3090	61	3150
CGCGCGCCGCGCCGCAAGAGGTGACTTCATCCAGGTGCAAGCTCCAGCCATCTGGC	CGCGCGCCGCGCCGCAAGAGGTGACTTCATCCAGGTGCAAGCTCCAGCCATCTGGC	CAGGCGCTGACTGTCTCGAGGCGAGCCCGACCTCAACGCGCTACAGTCACTGCAAGGTGG	CAGGCGCTGACTGTCTCGAGGCGAGCCCGACCTCAACGCGCTACAGTCACTGCAAGGTGG
60	314	120	320
CGCGCGCCGCGCCGCAAGAGGTGACTTCATCCAGGTGCAAGCTCCAGCCATCTGGC	CGCGCGCCGCGCCGCAAGAGGTGACTTCATCCAGGTGCAAGCTCCAGCCATCTGGC	CGCGCGCCGCGCCGCAAGAGGTGACTTCATCCAGGTGCAAGCTCCAGCCATCTGGC	CGCGCGCCGCGCCGCAAGAGGTGACTTCATCCAGGTGCAAGCTCCAGCCATCTGGC
121	3210	181	3270
GGGCTGAAGCGTACGCGCTCGCTAAAGCCGGAGCTACCCGCCCAACCATCTTTGCTCCC	GGGCTGAAGCGTACGCGCTCGCTAAAGCCGGAGCTACCCGCCCAACCATCTTTGCTCCC	CTTTCACATCCATGAAGCCCAATATGCGTGTAA	CTTTCACATCCATGAAGCCCAATATGCGTGTAA
180	326	216	3305
GGGCTGAAGCGTACGCGCTCGCTAAAGCCGGAGCTACCCGCCCAACCATCTTTGCTCCC	GGGCTGAAGCGTACGCGCTCGCTAAAGCCGGAGCTACCCGCCCAACCATCTTTGCTCCC	CTTTCACATCCATGAAGCCCAATATGCGTGTAA	CTTTCACATCCATGAAGCCCAATATGCGTGTAA

RESULT 6
US-09-957-187-3

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: Publication No. US2003005451A1
: GENERAL INFORMATION:
: APPLICANT: Larochelle, William A.
: APPLICANT: Shinkets, Richard A.
: TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
: FILE REFERENCE: 15966-540 CIP
: CURRENT APPLICATION NUMBER: US/09/957,187
: CURRENT FILING DATE: 2000-09-19
: PRIOR APPLICATION NUMBER: 60/123,667
: PRIOR FILING DATE: 1999-03-09
: PRIOR APPLICATION NUMBER: 09/520,781
: PRIOR FILING DATE: 2000-03-03
: PRIOR APPLICATION NUMBER: 60/234,082
: PRIOR FILING DATE: 2000-09-20
: PRIOR APPLICATION NUMBER: 60/233,798
: PRIOR FILING DATE: 2000-09-19
: PRIOR APPLICATION NUMBER: 60/174,485
: PRIOR FILING DATE: 2000-01-04
: NUMBER OF SEQ ID NOS: 85
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 3
: LENGTH: 3438
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (214)..(3030)
: NAME/KEY: misc. feature
: LOCATION: (3047)
: OTHER INFORMATION: an n may be any one of a o r t o r g o r c
: US-09-957-187-3

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Query Match	100.0%	Score 216;	DB 11;	Length 3498;
Best Local Similarity	100.0%	Pred. No. 5.5e-58;		
Matches 216;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0.

QY	1	CCGCGCGCGCGCGCGCAGAGGGGTGGACGTCACATCCAGAGGAGCAAGAGTCCAGGACTCTGGC	60
Db	3090	CCGCGCGCGCGCGCGCAGAGGGGTGGACATCCAGGAGGAGCAAGAGTCCAGGACTCTGGC	314
QY	61	CAGGCGCTGACTGTTCTCAGAGCAGCGCCAGCCTCAAGCGCTTACACTCACTGCAAGGTGC	120
Db	3150	CAGGCGCTGACTGTTCTCAGAGCAGCGCCAGCCTCAAGCGCTTACACTCACTGCAAGGTGC	320
QY	121	GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCGCCAAACCATCTTCTGCTCC	180
Db	3210	GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCGCCAAACCATCTTCTGCTCC	326
QY	181	CTTTCACATCCATGAAGCCCAATGATGGCTATACA	216
Db	3270	CTTTCACATCCATGAAGCCCAATGATGGCTATACA	3305

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/ RESULT 7
/ US-09-957-187-84
/ Sequence 84, Application US/09957187
/ Publication No. US2003005451A1
/
/ GENERAL INFORMATION:
/ APPLICANT: Shinkets, Richard A.
/ APPLICANT: Larochehelle, William
/ TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
/ FILE REFERENCE: 15966-540 CIP
/
/ CURRENT APPLICATION NUMBER: US/09/957,187
/ CURRENT FILING DATE: 2000-09-19
/ PRIOR APPLICATION NUMBER: 60/123,667
/ PRIOR FILING DATE: 1999-03-09
/ PRIOR APPLICATION NUMBER: 09/520,781
/ PRIOR FILING DATE: 2000-03-03
/ PRIOR APPLICATION NUMBER: 60/234,082
/ PRIOR FILING DATE: 2000-09-20
/

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PRIOR APPLICATION NUMBER: 60/233,798
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 60/174,485
PRIOR FILING DATE: 2000-01-04
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 84
LENGTH: 4250
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (250)..(3390)
US-09-957-187-84

Query Match 100.0%; Score 216; DB 11; Length 4250;
Best Local Similarity 100.0%; Pred. No. 5.7e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCGCGCGCGCGCGCGAGGCGTGGACTCCATCCAGGTCACAGCTCCAGCCATCTGGC 60
DB 3175 CCGCGCGCGCGCGCGAGGCGTGGACTCCATCCAGGTCACAGCTCCAGCCATCTGGC 3234
OY 61 CAGCGCGGAGCTGTCTGAGGACAGCCAGCTCAAGCCCTCACTACTGACAGGTG 120
DB 3235 CAGCGCGGAGCTGTCTGAGGACAGCCAGCTCAAGCCCTCACTACTGACAGGTG 3294
OY 121 GGGCTGAAGCGTACGCGCTGCTAAAGCGGAGCTACCCCAACCATCTTGTCTCC 180
DB 3295 GGGCTGAAGCGTACGCGCTGCTAAAGCGGAGCTACCCCAACCATCTTGTCTCC 3354
OY 181 CTTTCCATCCATGAAGCCCATGATGCTGTACA 216
DB 3355 CTTTCCATCCATGAAGCCCATGATGCTGTACA 3390

RESULT 8

US-09-918-995-3799/C
Sequence 3799, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 3799
LENGTH: 460
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(460)
OTHER INFORMATION: n = A,T,C or G
US-09-918-995-3799

Query Match 77.8%; Score 168; DB 11; Length 460;
Best Local Similarity 99.4%; Pred. No. 4.7e-43;
Matches 168; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 48 CCAGCCATCTGCGCCAGCCGCTGCTCTCCAGGACAGCCCACTCAAGGCTTACAATC 107
DB 459 CCAGCCATCTGCGCCAGCCGCTGCTCTCCAGGACAGCCCACTCAAGGCTTACAATC 400
OY 108 ACTGACAAGCTGGGGCTGAAGCTAGCGCTCTGCTAAAGCGGAGTACCCCAAAAC 167
DB 399 ACTGACAAGCTGGGGCTGAAGCTAGCGCTCTGCTAAAGCGGAGTACCCCAAAAC 340

OY 168 ATCCTTGTCTCCCTTCCACATCCATGAAGCCCAATGATCGGTACA 216
DB 339 ATCCTTGTCTCCCTTCCACATCCATGAAGCCCAATGATCGGTACA 291

RESULT 9

US-09-764-891-6944
Sequence 6944, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6944
LENGTH: 6767
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-891-6944

Query Match 25.5%; Score 55; DB 11; Length 6767;
Best Local Similarity 64.6%; Pred. No. 1.4e-07;
Matches 82; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

OY 74 TCTGAGGACAGCCAGCCTCAAGCCTCAAGCTCACTGACAGCAAGGTGGGGCTGAAGCTA 133
DB 5521 TCTGAGGACAGGAGGAGCTACACAGTATGACCTCTTCTGAGGAGCAAGAGGA 5580
OY 134 CGCCCTGCTTAAGCGGAGCTACCCCAACCATCTTGTCTTCCACATCA 193
DB 5581 CGCCCTGCTTAAGCTACCTGACCTGACCAAGGCTTCTTGTCTTCCACATCTG 5640
OY 194 TGAAGCC 200
DB 5641 TGAAGCC 5647

RESULT 10

US-09-764-891-6943
Sequence 6943, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6943
LENGTH: 6773
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-891-6943

Query Match 25.5%; Score 55; DB 11; Length 6773;
Best Local Similarity 64.6%; Pred. No. 1.4e-07;
Matches 82; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

OY 74 TCTGAGGACAGCCAGCCTCAAGCCTCAAGCTCACTGACAGCAAGGTGGGGCTGAAGCTA 133
DB 5527 TCTGAGGACAGGAGGAGCTACACAGTAATGCGACTTCTTGAAGAGGAGGA 5586
OY 134 CGCCCTGCTTAAGCGGAGCTACCCCAACCATCTTGTCTTCCACATCA 193
DB 5587 CGCCCTGCTTAAGCTACCTGACCTGACCAAGGCTTCTTGTCTTCCACATCTG 5646
OY 194 TGAAGCC 200


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QY      146 AGCGGAGCATCCCGCCCAACCATCTTGTGCTCCCGCTTCACATTCATGAAGCCCATG 205
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      212 CGCGCACCTTACGAGAAACCATTCACGGCTGCACCTCCACCTCAACCTCCACTG 271

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Search completed: September 30, 2003, 22:20:07
 Job time : 63.2004 secs